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- GRAY SCALE DOCUMENTS

### IMAGES ARE BEST AVAILABLE COPY.

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Perfect score:
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                Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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Sequence 11, Appl Sequence 9, Appli Sequence 9, Appli Sequence 12666, A Sequence 12506, Apple Sequence 24, Appl Sequence 21, Appl Sequence 21, Appl Sequence 11, Appl Sequence 26, Appl
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# ALIGNMENTS

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APPLICATION NUMBER: US/08/681,219
FILING DATE: 22-UTL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/48962/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
                                          TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Takaaki Sato and Junn Yanagisawa
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1185 Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                       amino acids
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1185 Avenue of the Americas
single
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GENERAL INFORMATION:

APPLICANT: Sato, Taka-Aki

TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON

TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION

FILE REFERENCE: 65823/JPW/PT

CURRENT APPLICATION NUMBER: US/10/092,138

CURRENT FILING DATE: 2002-09-06

NUMBER OF SEQ ID NOS: 33

SOFTMARE: Patentin Ver. 2.1

SEQ ID NO 9

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence
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                                                                                                         ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: source:synthesized
US-09-230-111C-9
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US-10-092-138-9
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Best Local Similarity luu.
                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 6
                                 Matches
                                                     Query Match
Best Local Similarity
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APPLICANT: Yanagisawa, Junn
APPLICANT: Yanagisawa, Junn
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOMAIN AND USES THEREOF
FILE REFERENCE: 48962-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,111C
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: source:synthesized
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100.0%; Pred. No. 6e+05;
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Pred. No.
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; ORGANISM: Streptomyces avermitilis US-10-156-761-12666
           CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR PILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/259,931
PRIOR APPLICATION NUMBER: 60/269,308
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
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Best Local Similarity
Matches 6; Conserva
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SEQ ID NO 12666
LENGTH: 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OMURA, SATOSHI
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SEQ ID NOS: 14110
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Zyskind, Judith W.
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HORIKAWA, HIROSHI
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Pred. No. 1.8e+02;
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Best Local Similarity
***ches 5; Conserva
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                                                                                                                  RESULT 7
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Sequence 24, Application US/10301997
Publication No. US20030148346A1
GENERAL INFORMATION:
APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12506
LENGTH: 329
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SEQ ID NO 5558
LENGTH: 322
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Best Local (
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Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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5; Conserv
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Zyskind, Judith W.
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83.3%;
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Pred. No.
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3.1e+02;
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RESULT 8
US-09-952-680A-19
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Best Local Similarity
Matches 5; Conserv
                                             Query Match
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Stanton, Marty
APPLICANT: Epstein, David
APPLICANT: Hamaguchi, No. US20030087239A1uko
TITLE OF INVENTION: Target Activated Biosensor and Methods of Using
FILE REFERENCE: 23239-501
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09952680A Publication No. US20030087239A1
      Matches
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CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 60/232,454
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 75
SOPTWARE: Patentin Ver. 2.1
                                                                                                   LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
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FILING DATE: 22-No. US20030148346A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/527,431
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/887,534
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/887,534
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/887,534
FILING DATE: <Unknown>
y Match 96.2%;
Local Similarity 83.3%;
hes 5; Conservative
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Rin-Laures; Li-Hsien REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America
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233 South Wacker Drive/6300 Sears Tower
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83.3%;
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Pred. No. 3.2e+02;
1; Mismatches 0
    Score 25; DB 11;
Pred. No. 3.5e+02;
1; Mismatches 0
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                                      Length 354;
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Query Match
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US-09-952-680A-21
                   RESULT 11
US-10-187-394-11
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                                                                                                                                                                                                                                                                                SEQ ID NO 589
LENGTH: 709
TYPE: PRT
Sequence 11, Application US/10187394
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Publication No. US20030204073A1
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Matches 5; Conservative
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SEQ ID NO 21
LENGTH: 354
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Publication No.
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APPLICANT: Epstein, David
APPLICANT: Hamaguchi, No. US20030087239Aluko
APPLICANT: Hamaguchi, No. US20030087239Aluko
TITLS OF INVENTION: Target Activated Biosensor and Methods of Using
FILE REFERENCE: 22239-501
CURRENT APPLICATION NUMBER: US/09/952,680A
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 60/232,454
PRIOR FILING DATE: 2000-09-13
NUMBER: OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lehmann-Bruinsma, Karin
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Version 2.1
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No. US20030087239A1
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Pred. No.
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Pred. No. 3.
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3.5e+02;
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                                                                                                                                                                                                     US-08-260-675-26
                                                                                                                                                                                                                            RESULT 12
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Matches
                                                                                                                                              Sequence 26, Application US/08260675
Publication No. US20030104993A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No. US20030176667A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/187,394
FILING DATE: 28-JUNE-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/496,398
FILING DATE: 02-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KECK, PETER
APPLICANT: SMART, JOHN
TITLE OF INVENTION: SIMPLE CHAIN ANALOGS OF
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
APPLICANT: COHEN, CHARLES M
TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND
TITLE OF INVENTION: REPAIR
                                                                             APPLICANT:
                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ ADDRESSEE: THIBEAULT, LLP
                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein LOCATION: 1..103 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
APPLICATION NUMBER: US 08/478,097
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                              RUEGER, DAVID C
KUBERASAMPATH, THANGAVEL
                                                                          OPPERMANN, HERMANN
OZKAYNAK, ENGIN
                                                          PANG, ROY HL
                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                      92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "BMP3 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STK-059CN
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Pred. No. 1.6e+02;
2; Mismatches 0;
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RESULT 13
US-10-050-050-26
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                                                                                                                                                                                         Sequence 26, Application US/100:
Publication No. US20030125230A1
GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/667,
PRILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/752,
PILING DATE: 30-AUG-1991
ATTORNEY_AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: C7, 829
REFERENCE/DOCKET_NUMBER: CR9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 55 ST
CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..104
OTHER INFORMATION: /note= "BMP3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                   APPLICANT: COOHEN, CHARLES M.
CHARETTE, MARC M.
KUBERASAMPATH, TH.
RUEGER, DAVID C.
                             TITLE
                                                                                                                                                                                                                                                                                                                            49 TIQSIV 54
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Similarity 66.7%;
4; Conservative
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                                                                                                                                                                                                                                Application US/10050050
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55 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
       SMART, JOHN E.
INVENTION: MORPHOGEN TREATMENT FOR LIMITING
PROLIFERATION OF EPITHELIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                            OPPERMANN, HERMANN
PANG, ROY H.L.
OZKAYNAK, ENGIN
SMART, JOHN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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Pred. No. 1.6e+02;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRP-070
                                                                                                                                        THANGAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 104;
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US-09-813-459-25
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Patent No. US20020107369A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
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FILING DATE: -dinknown>
APPLICATION NUMBER: US 08/445,882
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-074DV
TELECHONE: (508) 435-9001
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 5
                                                                                                                                                                                                                            Cunningham, No. US20020107369Aleen
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/050,050
FILING DATE: 15-Jan-2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                     APPLICANT: Lee, Se-Jin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 33
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                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: HOPKINTON STATE: MA
                                                                                                 ZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                   USA
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66.7%;
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Pred. No. 1.6e+02;
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Length 104; Indels

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CURRENT APPLICATION DATA:

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RESULT 15
US-09-813-459-26
; Sequence 26, Ap
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Patent No. US20020107369A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.3
Best Local Similarity 66.3
Matches 4; Conservative
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                                                                                                                                                                                                            COUNTRY: USA
ZIP: 90067
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,459
FILING DATE: 20-Mar-2001
CLASSIFICATION: CUNKNOWN>
             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/624,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/624,635
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
TELEPHONE: (619) 455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cunningham, No. US20020107369Aleen
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
LOCATION: 1..115
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lee, Se-Jin
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LOCATION:
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FILING DATE: 20-Mar-2001
CLASSIFICATION: <UNKnown>
TELEFAX: (619) 455-5110
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Pred. No. 1.8e+02;
2; Mismatches 0; Indels
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Search completed: November 26, 2003, 12:38:38 Job time: 10.8434 secs
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                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                              61 TIQSIV 66
                                                                                             1 TIQSVI 6
                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 115 amino acids TYPE: amino acid
                                                                                                                                                                                                                                NAME/KEY: Protein LOCATION: 1..115
                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                               CLONE: Murine GDF-10
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                              92.3%;
                                                                                                                            Score 24; DB 10; Length 115; Pred. No. 1.8e+02; 2; Mismatches 0; Indels
                                                                                                                             °.
                                                                                                                               Gaps
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Regult
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                 987654
                                                                                                                                                                                                                                                                                                                                                                                                                                    score
and is
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                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                 d. No. 18 the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beq
              A Geneseq_19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *
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                                   AAW50180
AAR44929
AAG00992
AAU34062
AAW97691
AAW976913
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Signal-transducing T. niveum Cyclospo Human secreted pro Staphylococcus aur Staphylococcus aur Staphylococcus aur Staphylococcus epi Human G-alpha-il a
                                                                                                                                                                                                                                                                                          Description
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	AAM51938	AAM51921			AAW36865				AAR60977	AARS		AAR46746							AAR47294			) AAY48452		×				) AAY43102	AAR51649	PAAB99036		ABB09275			AAB9906
growth 1	Human TGFbeta prot	Human TGFbeta prot	Human bone morphog	w	~	Human partial BMP-	Human BMP3 (fx) mor	Human BMP3 (fx). H	Human BMP3(fx). H	BMP3	BMP3 (fx).	Human BMP3 (fx) mo	Morphogen BMP3. H	Human BMP3 (fx) sev	BMP 3 finger-1-hee	Human BMP3 amino a	n BMP-3, S	14235 S		ğ	in CBMP-3.	Human prostate can	ent of	긆	domain of	fragme		<ul> <li>Bovine osteogenic</li> </ul>	Osteogenic unglyco	Human somatostatin	TSHR-Gs-alpha fusi	G protein-coupled	G protein-coupled	Human G-protein al	

# ALIGNMENTS

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RESULT 1
AAW50180
Inhibition; specific binding; signal-transducing protein; cytoplasmic protein; proliferation; cancer cell; apoptosis; virally infected cell.
                                                                                                                                                                                           Signal-transducing protein carboxy-terminal peptide.
                       WPI; 1998-145347/13.
                                        Sato
                                                                                         18-JUL-1997;
                                                                                                          12-FEB-1998.
                                                                                                                          WO9805347-A1.
                                                                                                                                          Synthetic.
                                                                                                                                                                                                            16-JUL-1998
                                                                                                                                                                                                                               AAW50180;
                                                                                                                                                                                                                                             AAW50180 standard; peptide; 6 AA
                                                                        22-JUL-1996;
                                                       (UYCO ) UNIV COLUMBIA NEW YORK.
                                      'n
                                      Yanagisawa J;
                                                                                                                                                                                                            (first entry)
                                                                        96US-0681219.
                                                                                         97WO-US12677
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Inhibition of signal transduction - by inhibiting binding between a signal-transducing protein and a cytoplasmic protein, for treating

viral infection

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biotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel composition is capable of inhibiting specific binding between a signal-transducing protein (STP) having the carboxy-terminal sequence (Ser/Thr)-Xaa-(Val/Ile/Leu), where Xaa = any amino acid (e.g. the present peptide), and a cytoplasmic protein (CP) containing the sequence AAW50162 or AAW50163. The composition can be used to inhibit the proliferation of cancer or virally infected cells, or induce apoptosis in cancer or virally
             cyclosporin by transforming a vector containing this sequence to a recombinant host. This allows effective production
                                         peptide bi
molecules.
                                                                                                                                     Isolated DNA sequence - which codes synthetase like activity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzyme; cyclosporin; synthetase-like activity; Tolypocladium niveum; T. inflatum GAMS; biosynthesis; vector; cyclosporin synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T. niveum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR44929
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                                                                                       This sequence represents an enzyme which has cyclosporin synthetase-
                                                                                                                Claim 1;
                                                                                                                                                                           N-PSDB; AAQ54386
                                                                                                                                                                                                                                                                                                                      09-JUL-1992;
                                                                                                                                                                                                                                                                                                                                             05-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                     12-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                  Tolypocladium niveum
                                                                                                                                                                                      WPI; 1994-010432/02
                                                                                                                                                                                                                                                                                              08-MAR-1993;
29-APR-1993;
                                                                                                                                                                                                             Leitner E,
                                                                                                                                                                                                                                                (SANO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infected
                                      like activity. This sequence was isolated from Tolypocladium (formerly known as T. inflatum GAMS). This enzyme catalyses to eptide biosynthesis of cyclosporins and structural catated molecules. This sequence may be used for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
   cyclosporin
                                                                                                                                                                                                                                   SANDOZ LTD.
SANDOZ PATENT GMBH.
SANDOZ-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIQSVI
                                                                                                              Page 41-84; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIQSVI 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclosporin synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AA;
                                                                                                                                                                                                             Schneider E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                   92AT-0001403.
93AT-0000437.
93CH-0001310.
93CH-0001375.
                                                                                                                                                                                                                                                                                                                                             93EP-0810474.
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                                                                                                                                                                                                             Schoergendorfer
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                   for
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                                                                                                                                                   enzyme
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                                                                                                                                                                                                              Weber
                                                                                                                                                  having cyclosporin
                this sequence in roduction of anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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RESULT 3
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ID AAG00902
XX AAG00902
XX AAG00
XX AAG0
DT 06-C
XX Huma
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                             of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
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                                                                                                                                                                                                                                                       regulatory sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; 5' EST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG00992 standard;
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TIQSII
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                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein,
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                                                                                                                             96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duclert A,
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                                                                                                     Score 25; DB 21;
Pred. No. 1.1e+02;
1; Mismatches 0;
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Pred. No.
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                                                                                                                                                                                                                                                          expression and secretion vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d sequence tag (5' EST) for correspond to 5'ESTs and for chromosome mapping procedures
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                                                                                                                                                     Length 89;
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                                                                                                       Gaps
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RESULT 4
AAU34062
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                                                                                                                                  The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC genes themselves and the encoded proteins. The prokaryotes used are CC genemoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used CC inventify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC programmes. The antisense nucleic acid sequence is also useful to screen CC a wide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein.

CC The protein acids which are required for cell proliferation in CC essential prokaryotic cellular proliferation protein.

CC fine printed specification, but was obtained in electronic format directly from WIPO at
                                                                 Matches
                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253655P.
22-DEC-2000; 2000US-257931P.
                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Seq ID No 5558; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck R,
Yamamoto RT,
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                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
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DB; AAS51921.
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TiQSVV 131
                                TIQSVI 6
                                                                                                                                322 AA,
                                                                 Conservative
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Xu HH;
                                                                              96.2%;
83.3%;
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                                                             Score 25; DB:
Pred. No. 4.6e.
1; Mismatches
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                                                                              DB 22;
4.6e+02;
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                                                                                              Length 322;
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                                                                 Indels
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RESULT 6
AAU36913
ID AAU3
XX
AC AAU3
XX
DT 14-F
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AAW97691
ID AAW9
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                                                                                                                                                                                                                                                                                                                       attenuated virulence were identified in a mouse model of bacteraemia. The nucleotide sequences of regions flanking the transposon insertion sites of these mutants were determined, and database sequence comparisons were performed to identify these virulence genes (see AAX07088-136) and the possible function of their protein products (see AAX07680-724). The P10C15 virulence gene product comprises the Cee AAX07680-136) and the possible function of their protein products of spartate semialdehyde dehydrogenase, a first ORF of P10C15 encodes the C-terminus of the aspartokinase 2 alpha subunit (see AAX07680). Both enzymes are involved in homoserine biosynthesis. A claimed method of identifying an antibacterial agent involves assaying potential agents for the ability to interfere with the expression of S. aureus virulence gene products. Also new is a S. cureus organism containing a functional mutation in one of the virulence genes, and its use in vaccine compositions.
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Best Local S
Matches 5
                                AAU36913;
                                                                 AAU36913 standard; Protein;
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the deduced amino acid sequence of the protein product of a virulence gene (see AAX07099) newly identified in Staphylococcus aumutant P14C15. S. aureus mutants containing chromosomal insertions
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N-PSDB; AAX07099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW97691 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibition of virulence for, e.g. screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacteraemia; aspartate semialdhyde dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virulence; P14C15;
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                                                                                                                                                                                                                        Local Similarity es 5; Conserv
                                                                                                                                                      128 TiQSVV 133
                                                                                                                                                                                       1 TIQSVI 6
                                                                                                                                                                                                                                                                                               329 AA;
                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                            96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes from Staphylococcus aureus potential anti-microbial agents
                                                                   329 AA
                                                                                                                                                                                                                          Score 25; DB 20;
Pred. No. 4.7e+02
1; Mismatches
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0;
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14-FEB-2002

(first entry)

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ABP40384
ID ABP4
XX
AC ABP4
XX
DT 24-J
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                                                                                                                                                                                                                                                                      RESULT
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CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC sequences.
                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-207727P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-253028P.
16-FEB-2001; 2001US-269308P.
24-JUL-2002
                                ABP40384;
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Seq ID No 12506; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-611495/70.
N-PSDB; AAS54772.
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Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus cellular proliferation protein #1083
                                                             ABP40384 standard;
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                                                                                                                                          riosvv 133
                                                                                                                                                                         TIQSVI 6
                                                                                                                                                                                                                                                                      329 AA;
                                                                                                                                                                                                        Conservative
   (first entry)
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Xu HH;
                                                               Protein; 332
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                                                                                                                                                                                                     Score 25; DB 22;
Pred. No. 4.7e+02;
1; Mismatches 0
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                                                                                                                                                                                                        0;
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RESULT 8
AAY94207
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABp355124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                  Human; G-alpha-i3; G protein; Gi protein; adenylyl dopamine; thyrotropin-releasing hormone; somatostat signal transduction pathway.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
24-JUN-1999;
                                                                           Homo sapiens
                                                                                                                                                        Human G-alpha-i3
                                                                                                                                                                                31-JUL-2000
                                                                                                                                                                                                          AAY94207;
                                                                                                                                                                                                                                AAY94207 standard; Protein; 354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              Specification, but USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID 5229; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABN92929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus antibacterial;
                        16-MAY-2000.
                                                 US6063626-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis ORF amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-381255/41
                                                                                                                                                                                                                                                                                                 131 TIQSVV 136
                                                                                                                                                                                                                                                                                                                        1 TiQSVI 6
                                                                                                                                                                                                                                                                                                                                                   <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                      332 AA;
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                               (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-055779P.
97US-064964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epidermidis; open reading frame; \mathsf{ORF}_i bacterial infection; gene therapy.
 99US-0339775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0134001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bush D;
                                                                                                                                                                                                                                                                                                                                                                96.2%;
                                                                                                                                                                                                                                                                                                                                                    ۳.
                                                                                                                                                                                                                                                                                                                                                                Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                  DB 23; Le
. 4.8e+02;
. hag 0;
                                                                                                                                                                                                                                                                                                                                                                             Length 332
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                              cyclase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infections
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RESULT 9
AAY85290
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Best Local Similarity
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New antisense compounds targeting nucleic acids encoding human G-alpha-il useful for modulating G-alpha-il expression and for treating diseases associated with G-alpha-il expression -
                                                                                             WPI; 2000-292434/25.
N-PSDB; AAA10854.
                                                                                                                                                                                                                                                          09-APR-1999;
                                                                                                                                                                                                                                                                                                     09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                04-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      delay, infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-alpha-il; G protein; adenylyl cyclase hormonal inhibition; tumour; plasma membrane regulation; antisense composition; treatment; preven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G-alpha-il amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY85290 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-alpha-i3 and can be used to prevent infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 14; Column 41-44; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compounds targeting nucleic acids encoding human G-alpha-I3 useful for treating diseases associated with G-alpha-I3 expression and as prophylaxis to prevent or delay infection, inflammation or tumor formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-375497/32.
N-PSDB; AAA15502.
                                                                                                                                                               Cowsert
                                                                                                                                                                                                                                                                                                                                                                                              US6046321-A
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77
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7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHARM INC
                                                                                                                                                                                                             PHARM INC
                                                                                                                                                                                                                                                          99US-0289377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation; tumour formation; research; diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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Pred. No.
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5.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation and
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The present invention describes a prodrug comprising a G-protein coupled receptor (GPCR). This can be used in

the treatment of

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RESULT 10
AAB99064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein coupled receptor; GPCR; GnRH receptor; disease treatment; gonadotrophin releasing; hormone receptor; hormone dependent cancer; human; catfish; goldfish; cow; sheep; horse; fruitfly; pig; rat; mouse;
                                                                            Use of a vector encoding G-protein coupled receptors for manufacturing medicaments for treating cancer, diseases of cardiovascular system, nervous system, digestive system, immune system, or muscle diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                  WPI; 2001-355607/37
                                                                                                                                                                                                                                                        17-NOV-1999;
                                                                                                                                                                                                                                                                                      17-NOV-2000; 2000WO-GB04385.
                                                                                                                                                                                                                                                                                                                          25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human G-protein alpha subunit il.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB99064 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 41-44; 31pp; English
                                                                                                                                                                                                                                                                                                                                                          WO200136446-A2
                                                                                                                                                                                                                      (UYBR-) UNIV BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                             therapy.
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5; Conserv
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                                            Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                        99GB-0027215
                                                19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                            78pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.2%;
                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 21;
Pred. No. 5.2e+02;
1; Mismatches 0;
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diseases, including hormone-dependent cancers, cardiovascular, nervous system, digestive system, immune system, respiratory, skeletal, endocrine, sensory and muscle diseases and disorders. The present sequence is a protein described in the exemplification of the invention.

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ARESULT 11
ARAB99
ARAB99
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XX
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                                                                                                                               Query Match
Best Local :
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Best Local
                                                                                                                                                                                                                                                         The present invention describes a prodrug comprising a vector encoding a G-protein coupled receptor (GPCR). This can be used in the treatment of diseases, including hormone-dependent cancers, cardiovascular, nervous system, digestive system, immune system, respiratory, skeletal, endocrine, sensory and muscle diseases and disorders. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 19; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of a vector encoding G-protein coupled receptors for manufacturing medicaments for treating cancer, diseases of cardiovascular system, nervous system, digestive system, immune system, or muscle diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-355607/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McArdle CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; catfish; goldfish; cow; sheep; horse; fruitfly; pig; rat; mouse;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-protein coupled receptor; GPCR; GnRH receptor; disease treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G-protein alpha subunit i3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2001
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  77
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                                                      1 TIQSVI 6
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                                                                                                    Similarity 5; Conserv
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5; Conser
TIQSII 82
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                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99GB-0027215
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                                                                                                                               96.2%;
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83
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                                                                                                    Score 25; DB
Pred. No. 5.2e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                               5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
5.2e+02;
                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                       Length 354;
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                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                       Gaps
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RESULT 12 ABB09273

ABB09275;

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RESULT 13
ABB09275
ID ABB09
XX
AC ABB09
                                                                                                                                                                                                                                                                                                                      The present invention describes a nucleic acid sensor molecule (I) comprising a target molecule activation site comprising a structure that recognises a target molecule and an optical signalling unit including at least one nucleotide coupled to a signalling molecule including at the compile of the target molecule. (I) is useful for identifying a pathological condition of (I) following (I) is useful for identifying a drug compound, by identifying a nucleic acid biosensor-based molecule profile of target molecules associated with a pathological condition or genetic alteration. (C) acid biosensor-based molecule profile of target molecules associated with a disease trait in a patient, administering a candidate compound to the patient, and monitoring changes in the profile. Alternately, the method convolves identifying a number of pathway target molecules, administering a candidate compound to a patient having a disease trait, and monitoring changes in the structure, level or activity of two or more of the pathway target molecules or the compared to the profile of target molecules or the compared to the profile of target molecules or the compared to the profile of a reference companies in the structure is compared to the profile of a reference detection of target molecule. (I) is also useful in multiple assays, for the applications and drug optimisation. The present sequence represents a comparation.
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Best Local (
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid sensor for detecting target molecule, comprises target molecule activation site and optical signaling unit that changes its optical properties upon allosteric modulation sensor after recognition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Target activated nucleic acid biosensor; signalling moiety; GPCR; nucleic acid sensor; detection; engineering; drug optimisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G protein-coupled receptor (GPCR) I1 SEQ
                                     ABB09275 standard; Protein; 354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 12; Page 89; 144pp; English
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                                                                                                                                                                                                                                                                                                                   invention.
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                                                                                                                              77 TiQSII 82
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                                                                                                                                                                                                   l Similarity
5; Conserv
                                                                                                                                                                                                                                                                               354 AA;
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                                                                                                                                                                                                                         96.2%;
83.3%;
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5.2e+02;
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RESULT 14
ABB56396
ID ABB56
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                                                                                                                                                                                                                                                                                                                                                                                                     CC comprising a target molecule activation site comprising a structure that CC recognises a target molecule and an optical signalling unit including at CC least one nucleotide coupled to a signalling molety that changes its CC optical properties upon allosteric modulation of (1) following CC optical properties upon allosteric modulation of (2) following crecognition of the target molecule. (1) is useful for identifying a pathological condition or genetic alteration. (CC (1) is useful for identifying a farget molecules associated with a patient, and monitoring changes in the profile of target molecules associated with CC addsease trait in a patient, administering a candidate compound to the Qualtent, and monitoring changes in the profile. Alternately, the method CC involves identifying a number of pathway target molecules, administering CC acandidate compound to a patient having a disease trait, and monitoring CC acandidate compound to a patient having a disease trait, and monitoring CC arget molecules using (1). The profile of target molecules or the CC changes in the structure is compared to the pathway target molecules or the CC changes in the structure is compared to the pathway target molecules or the CC changes in the structure is compared to the pathway target molecules or the CC changes in the structure is compared to the profile of a reference companies of target molecule. (1) is useful in multiple assays, for the detection of target molecule. (1) is also useful in diagnostic
                                                                                                                                                                                                                                                     Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid sensor for detecting target molecule, comprises target molecule activation site and optical signaling unit that changes its optical properties upon allosteric modulation sensor after recognition of target
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                                                      ABB56396;
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                                                                                         ABB56396 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-coupled receptor (GPCR) I3
                                                                                                                                                                                                                                                                                                                                                                                          protein-coupled receptor, which is used in an example from the present
                                                                                                                                                                                     77
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                                                                                                                                                                                                                                                                                                                                   354 AA;
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention describes a nucleic acid sensor molecule (I)
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                 (first entry)
                                                                                       Protein; 709
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Pred. No.
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to G protein-coupled receptors (GPCRs) for who the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a GPCR fusion protein containing thyroid stimulating hormone receptor (TSHR).
                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                    G-protein coupled receptor; GPCR; GnRH receptor; disease treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABI90836.
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constitutively activated GPCR; TSHR-Gs-alpha; TSHR-Gi-alpha; fusion;
                                                                                                        WO200136446-A2
                                                                                                                                                                                                                                                                         gonadotrophin releasing; hormone receptor; hormone
human; catfish; goldfish; cow; sheep; horse; fruitf
                                                                                                                                                                                                                                                                                                                                                                                          Human somatostatin receptor 2/Galphail fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           versions of GPCRs
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                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                              therapy
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83.3%;
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ses contacting candidate compounds with
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Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                            fruitfly; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 709;
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17-NOV-2000; 2000WO-GB04385

25-MAY-2001

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Search completed: November 26, 2003, 12:30:20 Job time : 17.6265 secs
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a prodrug comprising a vector encoding a d-protein coupled receptor (GPCR). This can be used in the treatment of diseases, including hormone-dependent cancers, cardiovascular, nervous system, digestive system, immune system, respiratory, skeletal, endocrine, sensory and muscle diseases and disorders. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 30-31; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of a vector encoding G-protein coupled receptors for manufacturing medicaments for treating cancer, diseases of cardiovascular system, nervous system, digestive system, immune system, or muscle diseases -
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448 TIQSII 453
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Pred. No. 1.1e+03;
1; Mismatches 0; Indels
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DDL BUCBP
BMP3 RAT
BMP3 HUMAN
BM3B MOUSE
BM3B RAT
                                                                                  DNAZ YEAST
POLG TMEVB
CDA2 YEAST
AQP7 MOUSE
DDL_BUCBP
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GB11
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POLG_TMEVD
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P08544
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ALIGNMENTS

#### YDEQ\_ECOLI 16-OCT-2001 (Rel. 4 16-OCT-2001 (Rel. 4 16-OCT-2001 (Rel. 4 Hypothetical fimbri YDEQ OR B1502 STRAINEKI / MG1655; MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; YDEQ\_ECOLI P77588; 16-OCT-2001 MEDININE-97251357; PubMed-9097039; Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Kashimoto K., Minura S., Kitakawa M., Kitagawa M., Makino K., Misi T., Mizobuchi K., Mori H., Mori T., Motomura K., Makino K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Wada C., Yamamot EMBL; AE000247; AAC74575.1; -. EMBL; D90792; BAA15175.1; -. EMBL; D90793; BAA15183.1; -. EMBL; D90793; BA6415183.1; -. PIR; A64904; A64904 EcoGene; EG13799; ydeQ. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Escherichia coli. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. SEQUENCE FROM N.A. STRAIN=K12; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997). SEQUENCE FROM N.A. NCBI\_TaxID=562; -!- SIMILARITY: TO TYPE-1 FIMBRIAL SUBUNITS. fimbrial-like STANDARD; . 40, Created) . 40, Last seq . 40, Last ann sequence update) annotation update) protein ydeQ precursor. 304 ₽ Burland V., yhew G.F., Ξ.

InterPro; IPR000259; Fimbrial.
Pfam; PF00419; Fimbrial; 1.
Hypothetical protein; Fimbria; Signal; Complete proteome.
SIGNAL 1 26 POTENTIAL.
CHAIN 27 304 HYPOTHETICAL FIMBRIAL-LIKE E

HYPOTHETICAL FIMBRIAL-LIKE PROTEIN YDEQ

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RESULT
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SMART; SM00275; G_alpha; 1.
GTP-binding; Transducer; ADP-ribo;
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InterPro; IPR001019; Gprotein_alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Guanine nucleotide-binding protein G(k), alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XENLA
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                                                                                                                                                                                                                                                                                               Pfam; PF00503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90346157; PubMed=2116977; Olate J., Martinez S., Purcell P.,
                                                                                                                                                                                                                                                                        PRINTS; PR00318; GPROTEINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma). The alpha chain contains the guanine nucleotide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: G proteins are composed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              involved as modulators or transducers in various transmembrane signaling systems. G(k) is the stimulatory G protein of receptor-regulated K(+) channels (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Guanine
                                                                                                                                                                                                                                                                                                                                                   $11046; RGXLI3.
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European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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ADP-RIBOSYL [1]
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RIBOSYL[1] (BY PARIBOSYL[1] (BY PARIBOSY
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38;
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ia; Pipoidea; Pipidae;
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01-OCT-1994
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INIT MET
LIPID
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SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNAI3
                                                                                                                                                                                                                                                   EMBL; D21234; BAA04766.1; HSSP; P10824; 1AS3.
                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
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NCBI_TaxID=10141;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                          between
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                                                                                                                                                                                                                                                                                                                                                                                  site.
TISSUE SPECIFICITY:
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                 signaling systems. G(k) is the stimulatory G protein of receptated K(+) channels. regulated K(+) channels composed of 3 units (alpha, beta and gamma). The alpha chain contains the guanine nucleotide bind:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              involved as modulators or transducers in various
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0; PubMed=1482697;
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ADP-RIBOSYL[1] (BY ACTION O
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Pred. No.
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Hystricognathi; Caviidae;
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RESULT 4
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Puhl H.L. III,
Submitted (MAR-
              Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malak J.A., Gunaratne P.H.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
McKernan K.J., Madan A., Rodrigues S., Sanchez A.,
McKernan M., Madan A., Rodrigues S., Sanchez A.,
McKetteman M., Madan A., Rodrigues S., Sanchez A.,
McKernan K., Madan A., Rodrigues S., Sanchez A.,
McKernan M., McKernan M., Madan A., Rodrigues S., Sanchez A.,
McKernan M., McKernan M., Madan A., Rodrigues S., Sanchez A.,
McKernan M., McKernan M., Madan A., Rodrigues S., Sanchez A.,
McKernan M., McKernan M., Madan A., Rodrigues S., Sanchez A.,
McKernan M., McKernan M., Madan A., Rodrigues S., Sanchez A.,
McKernan M., Mc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87247315; PubMed=3109953; Didsbury J.R., Snyderman R.; "Molecular cloning of a new human G. alpha-like protein families ", FEBS Lett. 219:259-263(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88247980; PubMed=3132707;
Kim S., Ang S.L., Bloch D.B., Bloch K.D., Kawal
Lee R., Seldman J.G., Neer E.J.;
"Identification of cDNA encoding an additional
human GTP-binding procein: expression of three
human tissues and cell lines.";
Proc. Natl. Acad. Sci. U.S.A. 85:4153-4157(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Alpha i-3 cDNA encodes the alpha subunit protein of receptor-regulated K+ channels J. Biol. Chem. 263:6746-6750(1988).
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"A small multigene family encodes Gi signal-transduction proteins.";

Proc. Natl. Acad. Sci. U.S.A. 84:7886-7890(1987).
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Birnbaumer L.;
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MEDLINE=88198230; PubMed=2834384;

Itoh H., Toyama R., Kozasa T., Tsukamoto T., Matsuoka M., Kaziro '
"Presence of three distinct molecular species of Gi protein alpha
subunit. Structure of rat cDNAs and human genomic DNAs.";

J. Biol. Chem. 263:6656-6664(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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MEDLINE=88198244; PubMed=2452165;
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Mammalia, Eutheria,
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protein G(k), alph
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e EMBL/GenBank/DDBJ
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-I- FUNCTION: Guanine nucleotide-binding proteins (G p involved as modulators or transducers in various t signaling systems. G(k) is the stimulatory G proteres regulated K(+) channels.

-I- SUBUNIT: G proteins are composed of 3 units (alpha gamma). The alpha chain contains the guanine nucle
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EMBL; M20598; AAA35895.1; JOII
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EMBL; M20601; AAA35895.1; JOII
EMBL; M20602; AAA35895.1; JOII
EMBL; M20602; AAA35895.1; JOII
EMBL; J03005; AAA35895.1; -
EMBL; J03198; AAA35895.1; -
EMBL; J03238; AAA35895.1; -
EMBL; AF493907; AAM12621.1; -
EMBL; BC025288; AAH25285.1; -
PJR; S02348; RGHUI3.
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GO; GO:000263; F:heterotrimeric G-protein GTPase, alpha-subunit;
GO; GO:0007194; P:negative regulation of adenylate cyclase ac. .
InterPro; IPR001019; Gprotein_alpha.
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RESULT 5
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RC STRAINS—25108163; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Arakawa T., Jara A., Rabhurner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Brownstein M.J., Bult C., Fletcher C., Füjita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Füjita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Mashima J., Mazzarelli J., Mombaerte P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schaefer C.F., Bhat N.K., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schaefer T.E., Ra Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Richards S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rosak S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Shevchenko Y., Bouffard G.G., A Hilting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G., A Hilting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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28-FEB-2003 (Re]
28-FEB-2003 (Re]
15-SEP-2003 (Re]
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97011591; PubMed=8858601;
Williams C.J., Schultz R.M., Kopf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF
STRAIN=CF-1
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                                                                                                                                                                                                                                                                                            protein gene expression during mouse protein gene expression during mouse
                                                SUBUNIT:
                                                                                   FUNCTION: Guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers in various transmembrane signaling systems. G(k) is the stimulatory G protein of receptor regulated K(+) channels (By similarity)
                                                                                                                                                                                                                                                     Reprod. Dev. 44:315-323(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247-321
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
leotide-binding protein G(k), alpha
                                           G proteins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harlan
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Rodentia;
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Sciurognathi; Muridae; Murinae; Mus
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of 3 units (alpha, beta and
the guanine nucleotide bind
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INIT MET
LIPID
                                                                           Jones D.T., Reed R.R.;

"Molecular cloning of five GTP-binding olfactory neuroepithelium.";
                                                          J. Biol.
                                                                                                                                                             SEQUENCE FROM N.A
MEDLINE=88007678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guanine nucleotide-binding GNAI3 OR GNAI-3.
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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GO; GO:0005794; C:Golgi apparatus; I
InterPro; IPR001019; Gprotein_alpha
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                                FUNCTION:
     involved as
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Eutheria; Rodentia;
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Kozasa T., Tsukamoto T., Matsuoka M.,
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                                                                                                              protein cDNA species
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Query Match
Best Local S
Matches
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01-OCT-1994
BIOCHIM. BIOPHYS. ACTA 1175:61-66(1992).

-I- FUNCTION: GUANINE NUCLECTIDE-BINDING PROTEINS INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIO SIGNALING SYSTEMS.
-I- FUNCTION: THE G(I) PROTEINS ARE INVOLVED IN HO
                                                                                                                                                                                                                                                        01-OCT-1994 (Rel. 30, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate cyclase-inhibiting G alpha protein).
                                                                                                                                                                                                                                                                                                                                                               CAVPO
                                                                   Sakanaka C., Izumi T., Nakamura M., Honda Z.-I., Watanabe T., Minami M., Mutoh H., Bito H., Seyama Y., Ui M., Shimizu T.; "Three types of Gi alpha protein of the guinea-pig lung: cDNA and analysis of their tissue distribution.";
                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIPID
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ProDom, PD000281; Gprotein_alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                             STRAIN=Hartley; TISSUE=Lung;
MEDLINE=93129640; PubMed=1482697;
                                                                                                                                                                                                                Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001019; Gprotein_alpha.
Pfam; PF00503; G-alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M20713; AAA40823.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institued in the modified and this statement
                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP-binding;
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                                                                                                                                                                                     CBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signaling systems. G(k) is the stimulatory G protein of receptor-regulated K(+) channels. SUBUNIT: G proteins are composed of 3 units (alpha, here and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: G proteins are gamma). The alpha chain
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83.3%;
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PALMITATE (BY SIMILARITY).

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ADP-RIBOSYL [1]
                                                                                                                                                                                                    Hystricognathi; Caviidae;
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the guanine nucleotide
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7E0F9 CRC64;
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                            TEINS (G
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                            PROTEINS) ARE TRANSMEMBRANE
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Best Local
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P50146;
                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Guanine nucleotide-binding protein G(i), alpha-1
cyclase-inhibiting G alpha protein).
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NP_BIND
MOD_RES
MOD_RES
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INIT_MET
LIPID
                                                   Kilbourne E.J., Galper J.B.;
"Cloning of cDNAs coding for the G alpha i
from chick brain.";
Gene 150:341-344 (1994)
-I- FUNCTION: GUANINE NUCLEOTIDE-BINDING I
INVOLVED AS MODULATORS OR TRANSDUCERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHICK
                                                                                                                                                                                                                                                                                                        Gallus gallus
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HSSP; P10824; 1AS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. Thuse by non-profit institutions as long
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                                                                                                                                                                                                                                                                   Archosauria; Aves;
                                                                                                                                                                                                                                                                                         Eukaryota;
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PRINTS; PR00318; GPROTEINA
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                                                                                                                                                     MEDLINE=95121926; PubMed=7821803;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                            CBI_TaxID=9031;
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                       SIGNALING FUNCTION:
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KIDNEY.
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THE ALPHA CHAIN CONTAINS
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ADRENERGIC STIMULI.
SUBUNIT: G proteins are composed of 3 units (alpha, beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHICK
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SM00275; G_alpha; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIQSII 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1PR001019; Gprotein_alpha
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                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 34, Created)
(Rel. 34, Last seq
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 SYSTEMS.
THE G(I)
CYCLASE:
                                                                                                                                                                                                                                                                                                      (Chicken)
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 PROTEINS ARE THEY INHIBIT
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PALMITATE (BY SIMILARITY).

GTP (BY SIMILARITY).

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GTP (BY SIMILARITY).

ADP-RIBOSYL[1] (BY ACTION OI

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 INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
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                                                         PROTEINS (G
IN VARIOUS
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IN THE BRAI
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                                                                                                                                                                                                                                                                   Phasianidae; Phasianinae;
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HORMONAL IN RESPONS
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BRAIN, LUNG
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                                                                                                                                   alpha
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                                                         PROTEINS) ARE TRANSMEMBRANE
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                                                                                                                                 G-proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L24548; AAA65066.1; -.
PIR; I50237; I50237.
HSSP; P10824; 1AS3.
InterPro; IFR001019; Gprotein_alpha
Pfam; PF00503; G-alpha; 1.
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                MEDLINE=87260939; PubMed=3110783; Bray P., Carter A., Guo V., Pucke
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                                                                                                                                    subunit.
                                                                                                                                                                                      MEDLINE=88198230; PubMed=2834384;
Itoh H., Toyama R., Kozasa T., Tsukamoto T., Matsuoka
                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606,
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                             Bos taurus
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                                                                        SEQUENCE
                                                                                                                  "Presence of three distinct molecular species of subunit. Structure of rat cDNAs and human genomion. Biol. Chem. 263:6656-6664(1988).
                                                                                                                                                                              Kaziro
                                                                                                                                                                                                                                                         SEQUENCE OF 1-100 FROM N.A.
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SUBUNIT: G
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nding; Transducer; ADP-ribosylation; Multigene family;
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ADP-RIBOSYL[1] (BY ACTION OF ADP-RIBOSYL[1] (BY ACTION OF ADP-RIBOSYL[1] (BY ACTION OF ADP-RIBOSYL[1]) (BY ACTION OF ADP-RIBOSYL[1])
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G(i), alpha-1 subunit (Adenylate
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                  Kamholz
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MIM; 139310; -.

MIM; 139310; -.

GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:000263; F:heterotrimeric G-protein
GO; GO:000263; F:heterotrimeric G-protein
GO; GO:000263; F:heterotrimeric G-protein
Interpro; IPR001019; Gprotein_alpha.

Pfam; PF00503; G-alpha; 1.

PRODOM; PR00318; GPROTEINA.

ProDom; PR000281; GPROTEINA.

PRODOM; PR000281; GPROTEINA.

PROMORT; SM00275; G alpha; 1.

SMART; SM00275; G alpha; 1.
                                                                                                                                                                                                                                                       EMBL; M20596; AAA35893.1; JOINED.

EMBL; M20594; AAA35893.1; JOINED.

EMBL; M20595; AAA35893.1; JOINED.

EMBL; M17219; AAA52581.1; -

EMBL; AF055013; AAC09361.1; -

EMBL; AF055013; AAC09361.1; -

EMBL; M3642; CAA77288.1; -

EMBL; M4207; AAA30561.1; -

PIR; A23631; RGBUII.

PIR; A28318; RGHUII.
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between
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FEBS Lett. 197:305-310(1986).
                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement or send an email to license@isb-sib.cl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michel T., Winslow J.W., Smith J.A., Seidman J.G., Neer E.J.; "Molecular cloning and characterization of cDNA encoding the "GTP-binding protein alpha i and identification of a related protein,
                                                                                       Myristate;
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Proc. Natl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
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Michel T., Winslow J.W., Smith J.A.,
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FUNCTION: THE G(I) PROTEINS ARE
ADENYLATE CYCLASE: THEY INHIBIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma).
THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1 (G(I/O/T/Z)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADRENERGIC
SUBUNIT: G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. Natl. Acad. Sci. U.S.A. 83:7663-7667(1986)
FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEIN
INVOLVED AS MODULATORS OR TRANSDUCERS IN VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
e; Palmitate; Lipoprotein; 3D-structure.

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39 46 GTP (BY SIMILARITY).
199 203 GTP (BY SIMILARITY).
268 271 GTP (BY SIMILARITY).
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OR TRANSDUCERS IN VARIOUS
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X MEDLINE-98055713; PubMed-9395335;

X MEDLINE-98055713; PubMed-9395335;

XA Oba Y., Yoshikuni M., Tanaka M., Mita M., Nagahama Y.;

A Oba Y., Yoshikuni M., Tanaka M., Mita M., Nagahama Y.;

RT "Inhibitory guanine-nucleotide-binding-regulatory protein alpha
RT gubunite in medaka (Oryzias latipes) occytes -- cDNA cloning and
RT decreased expression of proteins during oocyte maturation.";

RL Bur. J. Biochem. 249:846-853(1997).

CC -!- BIOCHEMS. GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS ARE INVOLVED IN HORMONAL
CC SIGNALING SYSTEMS. THE G(I) PROTEINS ARE INVOLVED IN HORMONAL
CC REGULATION OF ADENYLATE CYCLASE: THEY INHIBIT THE CYCLASE IN
CC RESPONSE TO BETA-ADRENERGIC STIMULI.
CC RESPONSE TO BETA-ADRENERGIC STIMULI.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS, ALPHA, BETA AND
CAMMA. THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING
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PRINTS; PRO0318; GPROTEINA.

ProDom; PD000281; Gprotein_alpha; 1.

SMART; SM00275; G_alpha; 1.

GTP-binding; Transducer; ADP-ribosylation; Multigene family;
Myristate; Palmitate; Lipoprotein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Guanine nucleotide-binding protein G(1), alpha-1 subunit (Adenylate Gyrlase-inhibiting G alpha protein) (Gi1 alpha subunit) (Gi alpha a.
                                                                                                                                                                            EMBL; AB001741; BAA19454.1; -. HSSP; P10824; 1AS3.
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                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                   InterPro; IPKUULUL.
Pfam; PF00503; G-al
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0503; G-alpha; 1.
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D -> E (IN REF.
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MOD_RES
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01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
Guanine nucleotide-binding protein G(i), al
cyclase-inhibiting G alpha protein).
                                                                                                                 "Structure of RG94 bound to AlF4-activated G(3 stabilization of the transition state for GTP Cell 89:251-261(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GBI1_RA;
 MEDLINE=98371012; PubMed=9705312; Posner B.A., Mixon M.B., Wall M.A "The A326S mutant of Gialphal as
                                                                                                                                                                                                                           Wall M.A., Coleman D.E., Lee Gilman A.G., Sprang S.R.;
                                                                                                                                                                                                                                                                           "Structures of active conformations of GTP hydrolysis."; Science 265:1405-1412(1994).
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88007678; PubMed=2820999;
Jones D.T., Reed R.R.;
"Molecular cloning of five GTP-bi
olfactory neuroepithelium.";
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MEDLINE=96107343; PubMed=8521505;
                                                                                                                                                                                                                                                                                                                    Coleman D.
                                                                                                                                                                                                                                                                                                                              MEDLINE=94353239; PubMed=8073283;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                          X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
MEDLINE=98447508; PubMed=9772163;
                                                                                                                                                                                                                                                                                                            Sprang S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                K-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
                                                  "Crystal structures of the G prot
and Mg2+: a crystallographic titr
dochemistry 37:14376-14385(1998)
                                                                                 Coleman D.E.,
                                                                                                                                                                                                                                                                                                                                        K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
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ADP-RIBOSYL(1) (BY A
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Pred. No.
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            M. A.,
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InterPro; IPKUULULI,
InterPro; IPKUULULI,
Pfam; PF00503; G-alpha; 1.
PRINTG; PR00318; GPROTEINA,
PRODOm; PD000281; Gprotein_alpha; 1.
SMART; SM00275; G_alpha; 1.
SMART; SM00275; G_alpha; 1.
SMART; SM00275; G_alpha; 1.
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SMART; SM01275; G_alpha; 1.
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PIR; C27423; RGRTI1.
PDB; 1GIA; 30-SEP-94
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PDB; 1GIT; 12-FEB-97
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FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.

FUNCTION: THE G(I) PROTEINS ARE INVOLVED IN HORMONAL REGULATION OF PUNCTION: THE G(I) PROTEINS ARE INVOLVED IN RESPONSE TO BETA-ADRENERGIC STIMULI.

SUBUNIT: G proteins are composed of 3 units (alpha, beta and
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1GIT;
1GFI;
1AGR;
1GDD;
1GG2;
1GP2;
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1AS2;
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1BH2;
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1CIP;
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CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE ONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1
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P27044;
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Olate J., Martinez S., Purcell P., Jorquera H., Codina J.,
Birnbaumer L., Allende J.E.;
"Molecular cloning and sequence determination of four diff
species coding for alpha-subunits of G proteins from Xenop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-OCT-1994 (Rel. 31, Last Sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Guanine nucleotide-binding protein G(i), alpha-1
cyclase-inhibiting G alpha protein).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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gamma).
THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE
SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1
                                                                                                SIGNALING SYSTEMS.
FUNCTION: THE G(I)
ADENYLATE CYCLASE:
                                                    ADRENERGIC STIMULI.
SUBUNIT: G proteins are composed of 3 units (alpha, beta and
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$ Lett. 268:27-31(1990).

$ LOTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G

FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G
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01-0CT-1996
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MEDLINE-95074921; PubMed=7983761;

Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pe
"Intragenomic linear amplification of human herpesvirus
suggests acquisition of oriLyt by transposition.";

J. Virol. 69:589-596(1995)

--- PUNCTION: THIS PROTEIN MAY AFFECT TRANSLOCATION OF T
GLYCOPROTEINS TO MEMBRANES. IT IS INVOLVED IN CAPSID
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                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ethe Buropean Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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ProDom; PD000281; Gprotein_alpha; 1.
SMART; SM00275; G_alpha; 1.
GTP-binding; Transducer; ADP-ribosylation; Multigene family;
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EMBL;
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PF00503; G-alpha;
L16947;
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and between the orbiviruses.";
Virus Res. 53:53-73(1998)
-!- FUNCTION: THE UPS PROTEIN IS ONE OF THE TWO PROTEINS
-!- GUNTITUTE THE VIRUS PARTICLE OUTER CAPSID.
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP5 FAMILY.
                                                                                                                                                                                                                        SEQUENCE 50
                                                                                                                                                                                                                                            Pfam; PF00901; Orbi_VP5; 1.
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a convergent the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.; "The complete sequence of four major structural proteins of horse sickness virus serotype 6: evolutionary relationships
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=98278331; PubMed=9617769;
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                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=86060;
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Pfam; PF01366; PRTP; 1.
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A; Molecule type: DNA
A; Residues: 1-15281 < WEB>
A; Residues: 1-15281 < WEB>
A; Cross-references: EMBL: Z28383; NID: g440168; PIDN: CAA82227.1;
A; Note: the mucleotide sequence was submitted to the EMBL Data
A; Note: only a part of the translation is shown
A; Note: the source is designated as Tolypocladium inflatum

PID:g440169 Library, November 1993

A;Status: nucleic acid sequence not shown

C;Superfamily: cyclosporin fungus cyclosporin synthetase; acetate-CoA ligase homology; a

ALIGNMENTS

#### C;Accession: B64640 C;Accession: B64640 R;Tomb, J.F., White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKennc son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997 Nature 388, 539-547, 1997 R, Hallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MUID:97394467; PMID:9252185 A; Accession: B64640 A; Status: preliminary; nucleic acid sequence not shown; translation not shown cyclosporin synthetase - cyclosporin fungus (;Species: Tolypocladium inflatum (cyclosporin fungus) C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 03-Nov-2000 C;Accession: S4587; S41309 C;Accession: S4587; S41309 Curr. Genet. 26, 120-125, 1994 Curr. Genet. 26, 120-125, 1994 A;Title: The peptide synthetase catalyzing cyclosporine production in Tolypocladium nive A;Reference number: S45487; MUID:95094306; PMID:8001164 A;Accession: S45487 A;Cross-references: GB:AE000605; GB:AE000511; NID:g2314103; PIDN:AAD08009.1; PID:g231410 C;Superfamily: acyl carrier protein homology C;Keywords: carrier protein F;78-148/Domain: acyl carrier protein homology <ACP> A; Molecule type: DNA A; Residues: 1-153 < TOM> acyl\_carrier protein - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 26-May-2000 B64640 Best Loc Matches Query Match Local 83 1 TIQSVI 6 Similarity 6; Conserve TIQSVI 88 Conservative 100.0%; 0 Score 26; DB Pred. No. 19; O; Mismatches DB 2; Length 153; 0 Indels 0 Gaps 0

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hypothetical protein PH1681 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: A71049
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C;Species: Caenorhabditis elegans
C;Decies: C-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
C;Accession: T28918
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  R;Kawarabayasi, Y.; Sawada, M.; Ohfuku, Y.; Funahashi,
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;14213-14676/Domain: acetate-CoA ligase homology <AL11>
;14698-14765/Domain: acyl carrier protein homology <AC11>
;1060,2558,4045,5537,7034,8094,9589,11086,12158,13654,14729/Binding site: phosphopantet
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4601-5057/Domain: acetate-CoA ligase homology <ACP4>
5506-5573/Domain: acyl carrier protein homology <ACP4>
6094-6546/Domain: acetate-CoA ligase homology <ACP5>
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acetate-CoA ligase homology <ACL6>
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Se: strain Bristol N2; clone C13F10
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oA ligase homology <ACL1>
Horikawa, H.; Haikawa, Y.; Hino, Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,</u>
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Pred. No.
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Pred. No. 2.9e+03;
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  Y.; Yamamoto, S. J.; Kushida, N.;
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probable adhesin [imported] - Bscherichia coli (strain 0157:H7, substrain RIMD ()Species: Escherichia coli (c)Species: Escherichia coli (c)Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 ()Accession: C90892 (R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.;
                                                                                                                                                                                       A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A64904
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.A.; Rose, D.J.; Mau, B.; Sh
Science 277, 1453-1462, 1997
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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A;Residues: 1-213 <KAW>
A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30793.1; PID:g3258110
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A;Accession: A71049
A;Status: preliminary; nucleic acid
C; Superfamily:
                                                              A;Cross-references: GB:BA000007; PIDN:BAB35530.1; PID:g13361573; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                   A; Reference number: A99629; A; Accession: C90892
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A; Residues: 1-304 <BLAT>
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5; Conserv
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5; Conserv
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                                                                                                                                                                                                                                                   Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.;
Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.;
    fimbrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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  protein fimH
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83.3%;
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1; Mismatches
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Pred. No.
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75;
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Shinagawa, H.
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Query Match

Score 25;

DB

2

Length 304;

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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; I iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou Nature 409, 529-533, 2001

A,Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: F85725
                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Molecule type: CMR>
A;Residues: 1-329 <KUR>
A;Cross-references: GB:BA000018; PID:g13701191; PIDN:BAB42486.1; GSPDB:GN00149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: 189916

R;Kuroda, M.; Ohta, T.; Uchlyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, Ma; A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimi C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: B89916
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A;Cross-references: GB:AE005174; NID:g12515169; PIDN:AAG56266.1; GSPDB:GN00145; UWGP:Z22A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable adhesin, FimH type protein Z2206 [imported] - Escherichia coli (strain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: F85725
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C;Species: Ca
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C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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                                                         T34450
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Best Local
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             al protein T19H12.4 - Caenorhabditis elegans
Caenorhabditis elegans
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5; Conservative
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2 TVQSVI 297
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ilarity 83.3%;
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Pred. No.
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Pred. No.
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Potamousis,
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K.; Apodaca
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                           GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting)

(Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterot

(Species: Homo sapiens (man)

(C) Pate: 31-Dec-1992 #sequence_revision 22-Nov-1996 #text_change 19-Jan-2001

(C) Accession: A28318, D28154; T08669

R; Bray, P.; Carter, A.; Guo, V.; Puckett, C.; Kamholz, J.; Spiegel, A.; Nirenbe

Proc. Natl. Acad. Sci. U.S.A. 84, 5115-5119, 1987

A; Title: Human cDNA clones for an alpha subunit of Gi signal-transduction prote
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ж;rrtre: нuman cDNA clones for an alpha subunit of Gi signal-transduction protein.
A;Reference number: A28318; MUID:87260939; PMID:3110783
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A;Cross-references: GB:X56090; NID:g64709; PIDN:CAA39570.1; PID:g64710
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay ains. The beta and gamma chains, required for GFDase activity, appear to be common to all rase; it is specific for each type of G protein.
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal rec;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transduction F;31-38/Region: nucleotide-binding motif A (P-loop)
F;360-263/Region: GTP-binding NKXD motif
F;37/Binding site: GTP (Tys) #status predicted
F;169/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
F;342/Modified site: ADP-ribosylarginine (Cys) (by pertussis toxin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Molecular cloning and sequence determination of four different cDNA species co-
A,Reference number: S11045; MUID:90346157; PMID:2116977
A,Accession: S11046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP-binding regulatory protein Gi alpha-3 chain (adenylate cyclase-inhibiting) - N;Alternate names: GTP-binding regulatory protein Gk alpha chain; guanine nucleo C;Species: Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U97009; PIDN:AAC69029.1; GSPDB:GN00023; CESP:T19H12.4 A;Experimental source: strain Bristol N2; clone T19H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-342 < DAV >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosm
A;Reference number: Z21528
A;Accession: T34450
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A; Residues: 1-345 < OLA>
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                                                                                                 Query Match
Best Local S
Matches 5
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Pred. No. 86;
1; Mismatches
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A.; Nirenberg,

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C;Paccession: A23631; A25888
C;Accession: A23631; A25888
R;Nukada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Haga, K.; Haga, T.; Ichiyama, A.; KaR;Nukada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Haga, K.; Haga, T.; Ichiyama, A.; KaRES Lett. 197, 305-310, 1986
REBS Lett. 197, 305-310, 1986
A;Title: Primary structure of the alpha-subunit of bovine adenylate cyclase-inhibiting A;Reference number: A23631; MUID:86136587; PMID:2419165
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A;Note: DKFZp564K1216.1

C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation;
E;254/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MA
E;40-47/Region: nucleotide-binding motif A (P-loop)
E;269-272/Region: GTP-binding NKXD motif
E;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
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C; Comment: The Gi alpha chain is specific for G protein that is involv
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A;Molecule type: mRNA
A;Residues: 106-112,'S',114-329,'N',331-336,'E',338-354 <MIC>
A;Cross_references: GB:M14207; NID:g163129; PIDN:AAA30561.1; PID:g163130
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A;Map position: 7g21-7g21
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A; Molecule type: mRNA
                                                                                                                                              A; Title: Molecular cloning and characterization of cDNA encoding the A; Reference number: A94131; MUID:87017009; PMID:3094012
                                                                                                                                                                                                              A;Cross-references: GB:X03642; NID:g390; PIDN:CAA27288.1; R;Michel, T.; Winslow, J.W.; Smith, J.A.; Seidman, J.G.; Proc. Natl. Acad. Sci. U.S.A. 83, 7663-7667, 1986
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A;Experimental source: fetal brain; clone DKFZp564K1216
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A;Residues: 'WGGCSAATGGSAAATVPRDSKPQTRDLGALSRAGKQSLVVRNSRPLLSAPLRTASPSTPLRKWWGRRGPRREAFE
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A; Residues: 1-101 < ITO>
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A; Residues: 1-354 < NUK>
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c;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay ains. The beta and gamma chains, required for GTPase activity, appear to be common to al rase; it is specific for each type of G protein.

C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal rey C;Superfamily: GTP-binding regulatory protein Gs alpha chain (C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nur;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MAT: F;40-47/Region: nucleotide-binding motif (GP) (in mature form) #status predicted F;2/Modified site: myristylated amino end (GI) (in mature form) #status predicted
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Best Local
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GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - rat N.Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterotrimeric C;species: Rattus norvegicus (Norway rat) C;bate: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 19-Jan-2001 C;Accession: C27423 J. Biol. Chem. 262, 14241-14249, 1987
A;Title: Molecular cloning of five GTP-binding protein cDNA species A;Reference number: A92614; MUID:88007678; PMID:2820999
A;Accession: C27423
A;Molecule type: mRNA
A;Residues: 1-354 <JON> C;Accession: C27423 R;Jones, D.T.; Reed J. Biol. Chem. 262, Reed, R.R. from rat olfactory

A;Cross-references: GB:M17527; NID:g203167; PIDN:AAA40825.1; PID:g203168
C;Comment: The G proteins are a family of guantine nucleotide-binding proteins that relay ains. The beta and gamma chains, required for GTPase activity, appear to be common to all rase; it is specific for each type of G protein.
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal rec;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nv F;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted CMAT>
F;269-272/Region: nucleotide-binding motif A (P-loop)

F;3/Binding site: palmitate (Cys) (covalent) #status predicted F;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #;F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted #status predicted

밁 S Query Match Best Local Matches 77 s S Similarity TIQSVI 6 Conservative 82 96.2%; ۲. Score 25; DB Pred. No. 88; Mismatches DB ۲, 0, Length 354,

RESULT 14

GTP-binding regulatory protein Gi alpha-1 chain (adenylate cyclase-inhibiting) - N;Alternate names: guanine nucleotide binding protein Gi alpha-1 chain; heterotri C;Species: Kenopus laevis (African clawed frog) C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 19-Jan-2001 C;Accession: S11045 C;Accession: S11045 Agrolate; J.; Martinez, S.; Purcell, P.; Jorquera, H.; Codina, J.; Birnbaumer, L.; heterotrimeric

A; Title: Molecular cloning and sequence determination A; Reference number: S11045; MUID:90346157; PMID:211697 FEBS Lett. 268, 27-31, 1990 PMID:2116977 different cDNA Allen

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A;Residues: 1-39 - ....
A;Cross-references: GB:J03220
R;Codina, J.; Olate, J.; Abramowitz, J.; Mattera, R.; Cook
R;Codina, J.; Olate, J.; Biol. Chem. 263, 6746-6750, 1988
J. Biol. Chem. 263, 6746-6750, 1988
A;Title: Alpha-i-3 cDNA encodes the alpha-subunit of G<sup>2</sup>K,
A;Title: Alpha-i-3 cDNA encodes the alpha-subunit of G<sup>2</sup>K,
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A;Cross-references; GB:X56089; NID:g64707; PIDN:CAA39569.1; PID:g64708
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay ains. The beta and gamma chains, required for GTPase activity, appear to be common to all rase; it is specific for each type of g protein
C;Comment: The Gi alpha chain is specific for G protein that is involved in hormonal reg
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation; nu
F;2-354/Product: GTP-binding regulatory protein Gi alpha-1 chain #status predicted <MATy
F;30-47/Region: nucleotide-binding motif A (P-loop)
F;30-272/Region: GTP-binding MXXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;3/Binding site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
F;351/Modified site: ADP-ribosylcysteine (Cys) (by pertussis toxin) #status predicted
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A;Residues: 1-354 «KIB:J03238; NID:g183686; PIDN:AAA35939.1; PID:g306822
A;Cross-references: G8:J03238; NID:g183686; PIDN:AAA35939.1; PID:g306822
R;Itoh, H.; Toyama, R.; Kozasa, T.; Tsukamoto, T.; Matsuoka, M.; Kaziro, Y.
J. Biol. Chem. 263, 6656-6664, 1988
A;Title: Presence of three distinct molecular species of G-i protein alpha-subunit.
A;Reference number: A28154; MUID:88198230; PMID:2834384
A;Accession: C28154
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A;Residues: 1-354 <DID:
A;Residu
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A; Residues: 1-354 < ITO>
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A;Residues: 1-334 <BEA>
A;Cross-references: EMBL:J03005; NID:g183183; PIDN:AAA52557.1; PID:g183184
R;Didsbury, J.R.; Snyderman, R.
PEBS Lett. 219, 259-263, 1987
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NiAlternate names: GTP-binding regulatory protein Gk alpha chain; guanine nucleotide
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5; Conserv
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; Pred. No. 88;
1; Mismatches
                                                                                                                                                                                                                               J.; Mattera, R.; Cook, R.G.; Birnbaumer,
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A;Map position: 1p13-1p13
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Superfamily: GTP-binding regulatory protein Gi alpha-3 chain #status predicted <MA
C;Keywords: blocked amino end; GTP binding; heterotrimer; lipoprotein; myristylation;
E;2-354/Product: GTP-binding regulatory protein Gi alpha-3 chain #status predicted <MA
E;40-47/Region: nucleotide-binding motif A (P-loop)
E;269-272/Region: GTP-binding MXXD motif
E;27/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
E;3/Binding site: myristylated amino end (Gly) (status predicted
E;178/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
E;351/Modified site: ADP-ribosylarginine (Cys) (by pertussis toxin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 'C',22-354 <SUK>
A;Residues: 'C',22-354 <SUK>
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relations: The beta and gamma chains, required for GTPase activity, appear to be common to a rase; it is specific for each type of G protein.
C;Comment: The G1 alpha chain is specific for G protein that is involved in hormonal rec;C;Genetics:
Search completed: November 26, Job time: 7.56627 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: S00078; MUID:87276552; A;Accession: S00078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The human genome encodes at least three non-allellic G proteins with alpha(i)-IA;Reference number: S00078; MUID:87276552; PMID:2440724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:119276; OMIM:139370
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Pred. No.
                                          12:35:57
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Maximum Match 100%
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Maximum DB
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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            SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrat:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_plant:*
11: sp_vortebrate
13: sp_virus:*
14: sp_unclassifi
15: sp_archeap:*
17: sp_archeap:*
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length: 2000000000
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Gapop 10.0 ,
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26
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118.334 Million cell updates/sec
         Match
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sp_rodent:*
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                                                                                                                                                                                                                                                     Q91119 streptomyce
Q91149 streptomyce
Q99164 tolypocladi
Q90713 anastrepha
1066001 oenococcus
Q001714 anastrepha
Q28945 sus scrofa
Q28945 sus scrofa
Q28945 ous scrofa
Q28976 uncultured
Q86mc7 oceanobacil
Q9f7f6 uncultured
                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                       025615 helicobacte
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         DARRE PRESENTATION SOCIETY OF THE PRESENTATION OF THE PRESENTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
025615
                                                                                                                     NATURE 388:539-547(1997).

A FUNCTION: THIS PROTEIN IS THE CARRIER OF THE GROWING FATTY ACID
CHAIN IN FATTY ACID BIOSYNTHESIS (BY SIMILARITY).

EMBL; ABOO0605; AAD08009.1; -
HSSP; P02901; 1ACP.
TIGR; HP0962; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           025615 PRELIMINARY;
025615;
01-JAN-1998 (TrEMBLrel. 05, C
01-JAN-1998 (TrEMBLrel. 05, L
01-OCT-2002 (TrEMBLrel. 22, L
Acyl carrier protein (ACP).
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STRAIN-26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Relson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Rolson K., Richardson D., Dodson R., Khalak H.G., Glodek A.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Hickey E.K.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Cotton M.D., Weidman J.M., Fujii C., Smith H.O., Fraser C.M.,

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,

Venter J.C.,
InterPro; IPR003231; Acyl_carrier.
InterPro; IPR006163; Pp_bind.
Pfam; PF00550; pp-binding; 1.
ProDom; PD00887; Acyl_carrier; 1.
TIGRPAMs; TIGR00517; acyl_carrier;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                            pylori.
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                                                                                                                                                                                                                                                                                    "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=210;
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Q8LYV7
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Q56591
Q843B7
Q9JGP5
Q8B0T5
Q8B0T5
Q8B0T6
Q9B0T7
Q9CN47
Q9CN47
Q94YE7
Q95YE7
Q94YE7
Q9
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Q9UGA4
Q8TAN5
Q90846
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Q22478
Q27XZ9
Q9TXZ9
Q9L6T5
Q9WWL2
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Last annotation update)
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Ogtan5 homo sapien
Ogoga6 ggallus ggall
Ogoga7 gallus ggall
Ogoga7 vibrio angu
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Fatty acid biosynthesis; Hypothetical protein; Phosphopantetheine; Complete proteome.
SEQUENCE 153 AA; 17917 MW; 5A1D715D9A394404 CRC64;
                                                                                                                        Pfam; PF00528; BPD
Sugar transport; Co
SEQUENCE 316 AA;
                                                                                                                                                                                                                           "Complete genome sequence coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=A3(2) / M14
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Cerdeno A.M., Parkhill J., 1
Submitted (FEB-2000) to the
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STRAIN=A3(2);
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InterPro; IPR000515; BPD_transp.
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transport; Complete proteome.
NCE 316 AA; 34367 MW; F4AK
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e EMBL/GenBank/DDBJ databases.
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InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR0016162; Ppantne_attach.
InterPro; IPR006163; Pp_bind.
InterPro; IPR00051; SAM bind.
Pfam; PF00501; AMP-binding; 11.
Pfam; PF00668; Condensation; 13.
Pfam; PF00650; pp-binding; 11.
                                                                                                                                                                                                                                                                                                PFAM, PF00550; pp-binding; 11.
PROSITE; PS0075; ACP_DOMAIN; 11.
PROSITE; PS00455; AMP_BINDING; 10.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUIT. Genet. 26:120-125(1994).

-i- FUNCTION: THE CONSTITUENT AMINO ACIDS OF CYCLOSPORINS ARE
-i- FUNCTIONED AS AMIONACYL-ADENYLATES WITH PEPTIDE BONDS FORMED
THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER INTERMEDIATES.
-I- COPACTOR: CONTAINS 11 COVALENTLY BOUND PHOSPHORANTETHEINES.
-i- COPACTOR: CONTAINS 11 COVALENTLY BOUND PHOSPHORANTETHEINES.
-i- PATHMAY: NON-RIBOSOMAL BIOGSYNTHESIS OF CYCLOSPORING.
-i- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weber G., Schoergendorfer K., Schneider-Scherzer E., Leitner E.; "The peptide synthetase catalyzing cyclosporine production in Tolypocladium niveum is encoded by a giant 45.8-kilobase open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota;
Hypocreales; Clavicipitaceae;
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HSSP; P14687; 1AMU.
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STRAIN=ATCC 34921;
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01-NOV-1998
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01-AUG-1998
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"A 24 kDa parasitism-specific protein from the Caribbean f Anastrepha suspensa: cDNA and deduced amino acid sequence. Insect Biochem. Mol. Biol. 29:749-755 (1999).

EMBL; AF165877; AAP101363.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anastrepha suspensa (Caribbean fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Anastrepha.
NCBI_TaxID=28587;
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01-MAY-2000
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
Parasitism-specific protein
                                                                                                                                   MEDLINE-98297285; PubMed-9633629;
Coton E., Rollan G.C., Lonvaud-Funel A.;
"Histidine carboxylase of Leuconostoc oenos
kinetic properties, cloning and nucleotide s
J. Appl. Microbiol. 84:143-151(1998).
                                                                                                                                                                                                                                                                             Oenococcus oeni (Leuconostoc oenos).
Bacteria; Firmicutes; Lactobacillales;
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                              Score 25; DB
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1; Mismatches
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Pred. No.
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Best Local S
Matches 5
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                                                                                                                                                                                                                           Q9U714
Q9U714;
Q9U714;
01-MAY-2000 (TEMBLrel. 13, C
01-MAY-2000 (TEMBLrel. 13, I
01-DEC-2001 (TEMBLrel. 19, I
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001488;
01-JUL-1997
01-JUL-1997
01-MAR-2003
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Hypothetical protein.
SEQUENCE 140 AA; 1
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WormPep; Cl3F10.2; CE08144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Direct Submission.";
Submitted (JUN-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tin A., Wohldmann P.;
"The sequence of C. e
Submitted (APR-1997)
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MEDLINE=99069613;
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                                                                                           SEQUENCE FROM N.A.
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                                                                                                                      NCBI_TaxID=28587;
                                                                                                                                                                                                                  Parasitism-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. investigating biology. The C. elega science 282:2012-2018(1998).
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83.3%;
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MEDLINE=99440192; PubMed=10510497; Shi X., Gomez S.P., Lawrence P.O.; "A 24 kDa parasitism-specific protein from the Caribbean fruit Anastrepha suspensa: cDNA and deduced amino acid sequence."; Insect Biochem. Mol. Biol. 29:749-755(1999). EMBL; AF165876; AAF01362.1; -.
                                                                                                                                                                          Anastrepha suspensa (Caribbean fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Tephritoidea; Tephritidae; Anastrepha.
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                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
PSP24.
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SEQUENCE
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., N. Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohu. Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., O. Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K. Masuchi Y., Shizuya H., Kikuchi H.; "Complete sequence and gene organization of the genome of a h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             059320;
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Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Aorta;
Ge T., Day N., Codina
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Sus scrofa (Pig).
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01-NOV-1996
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ProDom; PD000281; Gprotein_alpha; 1.
SMART; SM00275; G_alpha; 1.
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Mammalia; Eutheria;
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HSSP; P10824; 1GDD.
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Cetartiodactyla; Suina; Suidae;
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el. 07,
el. 20,
PH1681
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Pred. No. 1.2e
1; Mismatches
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MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from Ridge and its unexpected adaptive capabilities to extreme environments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9F7R6 PRELIMINARY; PRT; 265 AA.
Q9F7R6;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLREL 20, Last annotation update)
Q1-MAR-2003 (TrEMBLREL 20, Last annotation update)
Q1-MAR-2003 (TrEMBLREL 20, Last annotation update)
Q1-MAR-2003 (TrEMBLREL 20, Last annotation update)
Q2-MAR-2003 (TrEMBLREL 20, Last annotation update)
Q2-MAR-2003 (TrEMBLREL 20, Last annotation update)
Q3-MAR-2003 (TrEMBLREL 20, Last annotation update)
Q4-MAR-2003 (TrEMBLREL 20, Last annotation update)
                        Science 289:1902-1906(2000).
EMBL, AF279106; AAG10453.1; -.
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; lactamase_B; 1.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=20446260; PubMed=10988064;

Beja O., Aravind L., Koonin E.V., Suzuki M.T.,

Jovanovich S.B., Gates C.M., Feldman R.A., Spu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oceanobacillus iheyensis.
Bacteria, Firmicutes; Bac
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01-MAR-2003 (TrEMBLrel.
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EMBL; AP000006; BAA30793.1; -

Hypothetical protein; Complete proteome.

SEQUENCE 213 AA; 23516 MW; 7B57B54B27E71478
                                                                                                                                                 "Bacterial rhodopsin: evidence Sea.";
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RESULT 13
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                              O01609;
O01609;
O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-OCT-2001 (TrEMBLrel. 18, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hymothetical 37.0 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00419; Fim
Complete proteome.
SEQUENCE 304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Ohnishi M., Kurokawa K., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. B:11-22(2001).
EMBL; AE005354; AAG56266.1; -.
EMBL; AE005257; BAB35530.1; -.
InterPro; IPR00259; Fimbrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Putative adhesin, similar to FimH protein
Z2206 OR ECS2107.
Caenorhabditis elegans.
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STRAIN=0157:H7 / R
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MEDLINE=21074935; PubMed=11206551;
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Enterobacteriaceae; Escherichia.
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RESULT 14
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MEDIINE-1340416; PubMed-11447207;
Miltshire M.D., Foster S.J.;
Miltshire M.D., Foster S.J.;
Miltshire M.D., Foster S.J.;
Miltshire M.D., Foster S.J.;
Indect Inmun. 69:5198-5202(2001).
EMBL; AF306669; AAG42245.1;
InterPro; IPR005986; Asp. ADH USG1.
InterPro; IPR000534; Semialdh_dh.
Pfam; PF02118; Semialdhyde_dhc; 1.
Pfam; PF02774; Semialdhyde_dhc; 1.
TIGRFAMs; TIGR01296; asd B; 1.
TIGRFAMs; TIGR01296; asd B; 1.
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O9EZ13;
O9EZ13;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequ
O1-OCT-2002 (TrEMBLrel. 22, Last anno
Aspartate semialdehyde dehydrogenase.
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InterPro; IPR000276; GPCR Rhodgen.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
Hypochetical protein.
SEQUENCE 323 AA; 36972 MW; 076426D9
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=99069613; PubMed=9851916;
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NCBI_TaxID=6239;
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RESULT 15
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Q99U90;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Aspartate semialdehyde dehydrogenase.
ASD OR SAV1394 OR SA1226.
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Lancet 357:1225-1240(2001).
EMBL; AP003362; BAB57556.1; -.
EMBL; AP003133; BAB42486.1; -.
EMBL; AP003133; BAB42486.1; -.
InterPro; IPR005986; Asp ADH USG1.
InterPro; IPR005986; Asp ADH USG1.
InterPro; IPR005986; Semialdh dh.
Pfam; PF01118; Semialdhyde dh; 1.
Pfam; PF02774; Semialdhyde dh; 1.
TIGREAMS; TIGR01296; asd B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SPECIES=S.aureus (strain MuSO), and S.aureus (strain N315);

MEDLINE=21311952; PubMed=11418146;

MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879;
                                                                                                                                                                128 TIQSVV 133
                                                                                                                                                                                                                                                       1 TIQSVI 6
                                                                                                                                                                                                                                                                                                                                                                             96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36355 MW;
                                                                                                                                                                                                                                                                                                                                 Score 25; DB 16; Length 329;
Pred. No. 2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1B7F23140210B1E2 CRC64;
                                                                                                                                                                                                                                                                                                                                      0,
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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102.059 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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37
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
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                  US-10-032-201B-62
US-09-738-626-4130
US-10-144-156-18
US-09-876-348A-4
US-09-876-348A-3
US-09-876-348A-3
US-09-876-348A-27
US-09-876-348A-27
US-09-876-348A-27
US-09-876-348A-27
US-09-876-348A-27
US-09-876-348A-27
US-09-876-348A-27
US-09-876-348A-27
US-09-876-348A-27
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            Sequence 13, Appl
Sequence 11, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 27, Appl
Sequence 25, Appl
                                                                                                                                                                                                                                                                                                                                                                                             Description
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## ALIGNMENTS

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COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/681,219
FILING DATE: 22-UUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 0575/48962/JPW/JKM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
                                          TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 STREET: 1185 A
CITY: New York
STATE: New Yorl
                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                            ENGTH:
              amino acid
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1185 Avenue of the Americas
                            8 amino acids
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                                                                                                                                                                                                                                                                                                 Floppy disk
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Query Match
Best Local Similarity
Watches 8; Conserve
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Best Local Similarity
Thes 8; Conserve
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US-10-092-138-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-681-219-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-230-111C-11
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                                                                                                                       US-09-230-111C-11
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Publication No. US20030170723A1

GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
TITLE OF INVENTION: BICCHEMICAL PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: 65823/JUM/PT
CURRENT APPLICATION NUMBER: US/10/092,138
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09230111C Publication No. US20030203414A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, Junn
APPLICANT: Yanagisawa, Junn
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOMAIN AND USES THEREOF
FILE REFERENCE: 48962-A-PCT-US
CURRENT PILLING DATE: 1999-05-17
NUMBER: US/09/230,111C
CURRENT FILLING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:source:synthesized
                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                       TYPE: PRT
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  RETIESTV 8
                                         Conservative
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                                                         100.0%; Score 37; DB 12; 100.0%; Pred. No. 6e+05;
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Pred. No. 6e+05;
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Pred. No.
                                         Mismatches
                                                       6e+05;
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                                         US-09-738-626-4130
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Sequence 4130, Application US/09738626
Diblication No. US20020197605A1
GENERAL INFORMATION:
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                                                                                                                                                   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION UNMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION UNMBER: JF 99/377484
PRIOR FILING DATE: 199-12-16
PRIOR APPLICATION NUMBER: JF 00/159162
PRIOR APPLICATION NUMBER: JF 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JF 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Van Rooijen, Gijs
                                                                                                                   SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 4130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 62
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 193
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 38814 351B
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                                                           ORGANISM: Corynebacterium glutamicum
                                                                                                  LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 ŘETLEKTI 187
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                             IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moloney, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Del Val, Greg
Zaplachinski, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dalmia, Bipin Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deckers, Harm
Heifetz, Peter Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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81.1%;
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Pred. No. 92;
  Score 30;
  DB 10; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 193;
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APPLICANT: Horwath, K. L. and Myers, K. L.
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Typ
TITLE OF INVENTION: Artifreeze Proteins and Method for
FILE REFERENCE: RB-125-RI
CURRENT APPLICATION NUMBER: US/09/876,348A
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/210,446
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Microsoft Word
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ecker, Joseph R.
APPLICANT: Nehring, Ramlah
APPLICANT: NeGrath, Robert B.
TITLE OF INVENTION: ETHYLENE INSENSITIVE PLANTS
FILE REFERENCE: SALKINS.040A
CURRENT APPLICATION NUMBER: US/10/144,156
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 295
                                                RESULT 8
US-09-876-796A-4
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Best Local S
Matches 6
Sequence 4, Application US/09876796A Patent No. US20020173024A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                              ORGANISM: Tenebrio molitor
OTHER INFORMATION: Mature Protein for Tm 13.17
                                                                                                                                                                                                                                                                                                  LENGTH: 116
TYPE: PRT
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Similarity 85.7%;
6; Conservative
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62.5%;
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Pred. No.
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1; Mismatches 1
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Pred. No. 84;
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1.5e+02;
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Sequence 3, Application US/09876796A
Patent NO. US20020173024A1
GENERAL INFORMATION:
APPLICANT: HOTWARTH, K. L. and Easton, C. M.
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Typerite Reference: Ref-125-SEQ
CURRENT APPLICATION NUMBER: US/09/876,796A
CURRENT APPLICATION NUMBER: 00/210,446
PRIOR PILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 48
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US-09-876-348A-3
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Matches
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APPLICANT: HOTWATCH, K. L. and Myers, K. L.
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Type III Tenebrio
TITLE OF INVENTION: Antifreeze Proteins and Method for Assaying Activity.
FILE REFERENCE: RB-125-RI
CURRENT APPLICATION NUMBER: US/09/876,348A
CURRENT FILING DATE: 2001-08-09
CURRENT FILING DATE: 2001-08-09
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TITLE OF INVENTION: Aucleic Acid Sequences Encoding Type III Tenebrio
TITLE OF INVENTION: Aucleic Acid Sequences Encoding Type III Tenebrio
TITLE OF INVENTION: Aucleic Acid Sequences Encoding Type III Tenebrio
TITLE OF INVENTION: Aucleic Acid Sequences Encoding Type III Tenebrio Activity.
FILE REFERENCE: RB-125-SEQ
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/210,446
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Microsoft Word
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word SEQ ID NO 3
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SOFTWARE: Microsoft Word
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TYPE: PRT
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ORGANISM: Tenebrio molitor
OTHER INFORMATION: Mature Protein for Tm 13.17
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62.5%;
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62.5%;
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Pred. No. 99;
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Pred. No. 84;
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Query Match
Best Local Similarity
Watches 5; Conserve
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Best Local Similarity 62...
Conservative
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PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 48
SOFTWARE: MICROSOFT WORD
SEQ ID NO 27
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/09876796A
patent No. US20020173024A1
GENERAL INFORMATION:
APPLICANT: Horwath, K. L. and Easton, C. M.
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Antifreeze Proteins and Method
FILE REFERENCE: RB-125-SEQ
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Patent No.
                                                                                                                                                                                         SEQ ID NO 27
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TYPE: PRT
ORGANISM: Tenebrio molitor
OTHER INFORMATION: Mature Protein with His-tag, Tm 13.17
-09-876-348A-27
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CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/210,446
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Horwath, K. L. and Myers, K. L.
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Type III Tenebrio
TITLE OF INVENTION: Antifreeze Proteins and Method for Assaying Activity.
FILE REFERENCE: RB-125-RI
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                                                                                                                   TYPE: PRT
ORGANISM: Tenebrio molitor
OTHER INFORMATION: Mature Protein with His-tag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 134
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les 5; Conserv
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b. US20020172951A1
-1 RETIESTV 8
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62.5%;
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Pred. No.
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Pred. No.
                                                   Score 29;
Pred. No.
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                                                                 Length 149;
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RESULT 15
US-09-764-870-489
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US-09-876-796A-25
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SOFTWARE: Microsoft Word
SEQ ID NO 25
LENGTH: 174
TYPE: PRT
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US-09-876-348A-25
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Sequence 489, Application US/09764870
Patent No. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Nucleic Acids, Proteins, and Antibodies
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Patent No. US20020172951A1
GENERAL INFORMATION:
APPLICANT: Horwath, K. L. and Myers, K. L.
APPLICANT: HORWATION: Nucleic Acid Sequences Encoding Type III Tenebrio
TITLE OF INVENTION: Antifreeze Proteins and Method for Assaying Activity.
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Best Local Similarity
Matches 5; Conserv
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SEQ ID NO 25
LENGTH: 174
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Best Local (
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PRIOR FILING DATE: 2000-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Horwath,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/876,348A CURRENT FILING DATE: 2001-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: RB-125-RI
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Tenebrio molitor OTHER INFORMATION: Precurse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Tenebrio molitor OTHER INFORMATION: Precursor Protein with His-tag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                  Precursor Protein with His-tag, Tm 13.17
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                                                                                                                                                                                                                                                                       78.4%;
                                                                                                                                                                                                                                                     Score 29; DB 10;
Pred. No. 1.3e+02;
2; Mismatches 1
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Pred. No.
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Proteins and Method
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                                                                                                                                                                                                                                                                                         Length 174;
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FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Frior application data removed - consult PALM or file wrapper NUMBER OF 8EQ ID NOS: 646
SOFTWARE: PAtentin Ver. 2.0
SEQ ID NO 489
LENGTH: 199
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-870-489

Query Match
Best Local Similarity 71.4%; Score 29; DB 9; Length 199;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps O;
Search completed: November 26, 2003, 12:38:38
Job time: 14.4578 secs
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Listing first 45 summaries
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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Match
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Gapop 10.0 , Gapext 0.
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Copyright (c) 1993 - 2003
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AAU63147
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Compugen Ltd.
Signal-transducing Propionibacterium Arabidopsis thalia Arabidopsis th
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ID AAW5
XX AC AAW5
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                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibition; specific binding; signal-transducing protein; cytoplasmic protein; proliferation; cancer cell; apoptosis; virally infected cell.
                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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AAP90602
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AAR57365
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AAW65406
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Tml3.17 anti-freez
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RESULT 2
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The composition can be used to inhibit the proliferation of cancer or virally infected cells, or induce apoptosis in cancer or virally infected cells.
pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acmes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acme vulgaris. A method for detecting the
                                                                            Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                    Propionibacterium acnes polypeptides vaccinating against and diagnosing ir treating acne vulgaris -
                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                              L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW,
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02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes immunogenic protein #28398
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                                                                                                                                                                             Example 1; SEQ ID No 28697; 1069pp; English
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DB; AAS59529.
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re J, Zhang
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Jen S, Carter D;
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Pred. No.
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                                                                                                                                                                                                                                es and nucleic acids useful for infections, especially useful
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  RESULT 3
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XX AAG3
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DT 18-C
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Matches
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                                                                                                                                                                                                                  presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/jpublished_pct_sequences.
                                                                                                                                                                                   Sequence
                                                                                                               Local
24
                                         μ,
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                                                                                                               Similarity
                                         RETIESTV 8
RETSESTV 31
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                                                                                         Conservative
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Pred. No.
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40;
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Protein identification; signal transduction hybridisation assay; genetic mapping; gene of
                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                           AAG37884 standard; Protein; 193 AA.
termination sequence
                                                                                                                            18-OCT-2000
                                                                                                                                                                     AAG37884;
                                                                                                                          (first entry)
                                                                                  protein fragment
                                                                                  SEQ ID NO:
                                                                                     46656
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al transduction pathway; metabolic pathway;
mapping; gene expression control; promoter;

EP1033405-A2 Arabidopsis thaliana

21-APR-1999 23-APR-1999 23-APR-1999 28-APR-1999 30-APR-1999 30-APR-1999 04-MAY-1999 06-MAY-1999 06-MAY-1999 07-MAY-1999 11-MAY-1999 14-MAY-1999 14-MAY-1999 25-MAR-1999; 29-MAR-1999; 01-APR-1999; 19-APR-1999 08-APR-1999; 06-APR-1999; 23-MAR-1999 09-MAR-1999; 25-FEB-2000; 2000EP-0301439 06-SEP-2000 16-APR-1999; 99US-0130449 99US-0130077 99US-0130610 99US-0130891 99US-0131449 99US-0131491 99US-0132048 99US-0132407 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0134218 99US-0134219 99US-0134219 99US-0134219 99US-0134219 99US-0125788. 99US-0126264. 99US-0126785. 99US-0127462. 99US-0128234. 99US-0128714. 9905-0123548 99US-0121825

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26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
The present invention describes a method (M1) for producing an oil body associated with a recombinant multimeric protein complex (MPC). M1 comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (P1, P2), where P1 is capable of associating with P2 to form the MPC and associating the complex with an occlusion body (OB) through an OB-targeting-protein capable of associating with OB and P1. M1 is useful for producing an oil body associated with a recombinant MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care product which reduces the oxidative stress on the surface
                                                                                                                                                                                                Producing oil body associated with recombinant multimeric protein complex e.g. redox proteins and immunoglobulins comprises producing recombinant polypeptides capable of forming the complex in cells comprising oil bodies -
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                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-2000; 2000US-0742900.
05-JUL-2001; 2001US-302885P.
04-DEC-2001; 2001US-0006038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis; bronchiopulmonary disease; malignancy; reperfusion injury; wound healing; gastro intestinal bleeding; intestinal bowel disease; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multimeric protein; redox protein; thioredoxin; thioredoxin reductase; oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic; vasotropic; vulnerary; antibacterial; immunosuppressive; antilicer; food product; milk; wheat; oxidative stress; cataract; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP60713 standard; Protein; 193
                                                                                                                                                                    Claim 81; Page 214-215; 362pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-2001; 2001WO-US50240
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Val G, Zaplachinski
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99US-0161360.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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62.5%;
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Moloney M;
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Pred. No.
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Matches 5
06-APR-1999

16-APR-1999

119-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

06-MAY-1999

06-MAY-1999

06-MAY-1999

11-MAY-1999

11-MAY-1999
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               area of the human body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, envenomation, bronchiopulmonary disease, posriasis, malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (gastro oseophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to ABP60964 represent sequence given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybridisation assay;
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99US-0128234.
99US-0128714.
99US-0128715.
99US-0130477.
99US-0130510.
99US-013049.
99US-0131449.
99US-0132484.
99US-0132486.
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99US-0132487.
99US-0132487.
99US-0134256.
99US-0134256.
99US-0134256.
99US-0134218.
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99US-0123180.
99US-0123548.
99US-0125788.
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62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic mapping; gene expression control; promoter;
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Pred. No. 1.8e+02;
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	9US-013562 9US-013602 9US-013639 9US-013678
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05-AUG-1999 06-AUG-1999 11-AUG-1999 11-AUG	2-AUG-1993-AUG-1994-AUG-1994-AUG-1994-AUG-1994-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-AUG-1995-A
99US-014772 99US-0147733 99US-0147733 99US-0147733 99US-0148311 99US-0148341 99US-0148341 99US-0148341 99US-0148341 99US-0148341 99US-0149722 99US-0149722 99US-0149722 99US-0149902 99US-0149902 99US-0151065 99US-0151065 99US-0151333 99US-0151333 99US-0151333 99US-0151333 99US-0151333 99US-0151333 99US-0151333 99US-0151333 99US-0151333 99US-015925 99US-015925 99US-015925 99US-015925 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-015923 99US-016924 99US-016931 99US-016931 99US-016931 99US-016931 99US-016931 99US-016931 99US-016931 99US-016931 99US-016931 99US-016931 99US-0161363 99US-0161369 99US-0161369	9US-014638 9US-014703 9US-014720

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23-MAR 1999
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26-APR 1999
16-APR 1999
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21-APR 1999
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24-MAY 1999
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11-MAY 1999
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28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG37883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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RETLEKTI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana protein
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99US-0161993.
99US-0162142.
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62.5%;
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3-0123548.
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Pred. No. 1.9e+02;
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17-JUN-1999
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99US-0138540-0
99US-0138540-0
99US-0139452-0
99US-0139453-0
99US-0139456-0
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99US-0139460-0
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99US-0149461-0
99US-0149353-0
99US-0149368-0
99US-0149313-0
99US-014
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Query Match
Best Local S
Matches 5
h 81.1%;
Similarity 62.5%;
S; Conservative
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9903-0148341
9903-0148361
9903-0148684
9903-0149722
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99US-0147493.
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Score 30; DB 21; Length 217; Pred. No. 2e+02; 2; Mismatches 1; Indels
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AAG90376
RESULT 8
ABP57742
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                                                       Query Match
Best Local S
Matches 6
                                                                                    Sequence
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N-PSDB; AAH65595.
                                                                                                                                                                                                                                                                                                                     16-DEC-1999;
07-APR-2000;
                                                                                                                                                                                                     Claim 17;
                                                                                                                                                                                                                                                                           Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                               03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001
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                                                                                                                                                                                                                                                                                               (КҮОМ ) КҮОМА НАККО КОСУО КК
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                            41
                                                        Similarity 6; Conserv
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                                                                                     289 AA;
                                                        Conservative
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; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A, Ikeda
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Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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                                                               81.1%;
75.0%;
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da M,
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sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C glutamicum protein fragment SEQ ID NO: 4130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number
                            Score 30;
Pred. No.
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Ozaki A;
Mismatches
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                            2.8e+02;
                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listing; English.
                                                            Length 289;
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Indels
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Gape
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Best Local S
Matches 6
                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel BIN6 (ethylene insensitive 6) polynuclectide. The polynuclectide is useful in conferring an ethylene insensitive phenotype in plants, such as delayed ripening, flowering, delayed sensecence, browning, or altered sensitivity to pathogens, whice may improve the quality and longevity of many crops. The present sequent represents Y48B6A.11, a predicted protein from C. elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIN6; ethylene insensitive 6; ethylene; plant; delayed ripening; flowering; delayed senescence; browning; pathogen sensitivity; longevity; fruitfly; CG9088.
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                                                                                                                                                                                                                                              27-FEB-2002
                                                                                                                                                                                                                                                                                                                        AAU63147 standard; Protein; 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated EIN6 polynucleotide for conferring ethylene insensitive phenotype in plants, such as delayed ripening, flowering, delayed senescence or browning, which may improve quality and longevity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ecker JR,
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   01-NOV-2001
                                                                                                                                                                                                         Propionibacterium acnes immunogenic protein #24043.
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                                      WO200181581-A2.
                                                                         Propionibacterium acnes
                                                                                                                dermatological; osteopathic; neuroprotectant.
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1; Mismatches
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Best Local S
Matches 5
                                                                                                                                                                                                                                              31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                          07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS59632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW,
                   28-AUG-2001; 2001WO-EP09892
                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                     ABB93055;
                                                                                                                                                                                                                                                                                                                        ABB93055 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                   348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RETIESTV 8
                                                                                                                                                                                                                                                                                                                                                                                                                   REAVESTI 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Persing DH,
e J, Zhang
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presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
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02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                    Herbicidally active polypeptide SEQ ID NO 2266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID No 24342; 1069pp; English
Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                     Protein; 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides and nucleic acids useful for diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĸ
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, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 391;
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RESULT 11
AAU62952
ID AAU62
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
 Propionibacterium acnes vaccinating against and
                                                                                                Skeiky YAW,
                                                                                                                                                  21-APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                                                                                                                                                                                                                                                    dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                 WO200181581-A2
                                                                                                                                                                                                                                                                                          Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes immunogenic protein #23848.
                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU62952 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; SEQ ID NO 2266; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                   L'maisonneuve
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                                                                                                                           (CORI-) CORIXA CORP.
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                                            AAS59630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    herbicides.
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                                                                                Persing DH,
e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.1%;
polypeptides and nucleic acids useful for diagnosing infections, especially useful
                                                                                Mitcham JL, Wang SS, Jen S, Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 650;
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RESULT 12
ABU71056
ID ABU71
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C. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the yresence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining E. acnes presence, for example, by conversion, but was obtained in electronic format directly from WIPO are fire with out was obtained in electronic format directly from WIPO.
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Best Local
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                          New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obssity or diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides. The proteins and their associated DNA sequences the treatment, prevention and diagnosis of medical conditions P. acnes. The disorders include SAPHO syndrome (synovitis, acr
                                                                                                           WPI; 2003-103412/09.
N-PSDB; ACA57600.
                                                                                                                                                                                                                                                       14-MAR-2002; 2002WO-EP03768.
                                                                                                                                                                                                                                                                                                                       WO200286122-A2
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                    anorectic; antidiabetic; protein-protein interaction; diabetes;
yeast 2-hybrid assay; metabolic disorder; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prey; adipocyte; SID; selected interacting domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adipocyte Selected Interacting
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                                                                                                                                                                                                                         14-MAR-2001; 2001US-275734P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU71056 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
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                                                                                                                                                                                          HYBRIGENICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RETVESRI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU39105-AAU68017 represent Propionibacterium acnes des The proteins and their associated DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 24147; 1069pp; English
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                                                                                                                                                          Daviet
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A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 117
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62.5%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain,
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Claim 6; Page 343-344; 382pp; English

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RESULT 13
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Best Local S
Matches 6
                                               (UYNY )
(HORW/)
(MYER/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10036 standard; Protein; 134 AA.
 Horwath
                                                                                                                                          07-JUN-2001; 2001WO-US18532
                                                                                                                                                                           13-DEC-2001.
                                                                                                                                                                                                         WO200194378-A1
                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                     Tenebrio molitor
                                                                                                                                                                                                                                                                                                                                                                            Anti-freeze peptide; Tm 13.17; yellow mealworm beetle; THP; cryoinjury; thermal hysteresis protein; cryosurgery; cold climatisation; hypothermic cell preservation; de-icing formulation; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tml3.17 anti-freeze
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                                                                                                           08-JUN-2000; 2000US-210446F
                                                                                                                                                                                                                                                                                                                                                                  transgenic animal
                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 QTIESTV 60
                                               UNIV NEW YORK STATE RES HORWATH K L.
MYERS K L.
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                               EASTON C M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
Myers KL,
                                                                                                                                                                                                                                                        19..116
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                   /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.4%;
85.7%;
                                                                                                                                                                                                                                      "Mature Tm13.17 protein'
 Easton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB
Pred. No. 1.6e
1; Mismatches
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ARUIDIT 14
ARUIO049
ID AAUIO0
XX AAUIO
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XX 21-MA
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XX Anti-
KW Anti-
KW therm
KW hypot
KW trans
XX Tenek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                              thermal hysteresis protein; cryosurgery; cold climatisation; hypothermic cell preservation; de-icing formulation; transgenic plant; transgenic animal; His tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA libraries in an expression system, including cross-species cDNA libraries to identify homologous sequences in other species. The present sequence represents the Tm13.17 anti-freeze protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence encoding a thermal hysteresis protein ("HP) which is a Type III anti-freeze protein derived from the Tenebrionoidea Superfamily. Anti-freeze proteins lower the freezing point of a solution without affecting the melting point of the solution. An activated anti-freeze protein may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cDNA polynucleotide encoding a thermal hysteresis protein which is a Type III anti-freeze protein derived from the Tenebrionoidea Superfamily, useful for providing antifreeze protection to improve the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-090137/12
N-PSDB; AAS21109.
                                                                                                                                                                                                                                                                                                                                Anti-freeze peptide; Tm 13.17; yellow mealworm beetle; THP; cryoinjury;
                                                                                                                                                                                                                                                                                                                                                                             Tm 13.17 clone/His tag fusion protein minus signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU10049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10049 standard; Protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Fig 2.6a; 364pp; English.
                                                                                                             Protein
                                                                                                                                                                                                                       Tenebrio molitor.
                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to a cDNA polynucleotide comprising ing a thermal hysteresis protein (THP) which
                                                                    has been removed
                                                                                                               34..149
                                                                 /note= "Mature AFP protein, the signal sequence
has been removed for the purposes of cloning"
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                   /note= "Peptide including His tag'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.4%;
62.5%;
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Pred. No. 1
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1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 134;
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AAU76232
ID AAU76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a cDNA polynucleotide comprising a nucleotide cosquence encoding a thermal hysteresis protein (THP) which is a Type III canti-freeze protein derived from the Tenebrionoidea Superfamily. Anti-cc freeze proteins lower the freezing point of a solution without affecting the melting point of the solution. An activated anti-freeze protein may compressed into plant, produce or fish in an amount sufficient to provide antifreeze protection or in a region of a target tissue to provide antifreeze protein to limit tumour cell or target tissue to cryoinjury during cryosurgery. The proteins of the invention may also be used in hypothermic solutions or bathing media to reduce cold damage in cryosurger to provide cryogenic or hypothermic preservation of cells and corder to provide cryogenic or hypothermic preservation of cells and crissues. The proteins may be used as de-icing formulations or used on crisces to reduce existing ice buildup or shate the formation of ice buildup on surfaces such as a road, aircraft, household products, can be used by abating freezing of solutions, freezer burn, or degradation cold use to cold storage. The polynucleotides for the activated protein can be used to create transgenic or gene-modified plants, crops, fish, or cold cold having greater tolerance to cold climatisation. The Tm 12.86 cantibody/antiserum which is also used as a screening device to screen cold.
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches
Anti-freeze peptide; Tm 13.17; yellow mealworm beetle; THP; cryoinjury; thermal hysteresis protein; cryosurgery; cold climatisation; hypothermic cell preservation; de-icing formulation; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA libraries in an expression system, including cross-species cDNA libraries to identify homologous sequences in other species. The present sequence represents the Tm 13.17 clone/his tag fusion protein minus the signal peptide of the invention. This cDNA was created to try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cDNA polynucleotide encoding a thermal hysteresis protein which is a Type III anti-freeze protein derived from the Tenebrionoidea Superfamily, useful for providing antifreeze protection to improve the quality of food -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-090137/12.
N-PSDB; AAS21120.
                                                                                  Tm 13.17
                                                                                                                       21-MAY-2002
                                                                                                                                                           AAU76232
                                                                                                                                                                                                     AAU76232 standard; Protein; 174
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(EAST/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enhance the anti-freeze activity of the recombinant protein
                                                                                                                                                                                                                                                                                                   124
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MYERS K L.
EASTON C M.
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                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                             clone/His tag fusion protein #2
                                                                                                                                                                                                                                                                                                   RDTVEETV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 AA;
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                       (first entry)
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Pred. No. 2.1e+02;
2; Mismatches 1; Indels
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음 성

149

1 RETIESTV 8

Matches

5

Conservative

Query Match Best Local Similarity

78.4%; 62.5%;

Score 29; DB 23; Pred. No. 2.5e+02; 2; Mismatches 1

Length 174;

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Gaps

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cc sequence encoding a thermal hysteresis protein (THP) which is a Type III canti-freeze proteins lower the freezing proint of a solution without affecting the melting point of the solution. An activated anti-freeze protein may be incorporated into plant, produce or fish in an amount sufficient to provide antifreeze protein to limit tumour cell or target tissue to provide antifreeze protein to limit tumour cell or target tissue to cryoinjury during cryosurgery. The proteins of the invention may also be used in hypothermic solutions or bathing media to reduce cold damage in cryosurger to provide cryogenic or hypothermic preservation of cells and crisues. The proteins may be used as de-icing formulations or used on cold tissues. The proteins may be used as de-icing formulations or used on cold surfaces such as a road, aircraft, household products, cof food by abating freezing of solutions, freezer burn, or degradation cold used to create transgenic or gene-modified plants, crops, fish, or cold surfaces in an expression system, including cross-species cDNA collibraries in an expression system, including cross-species cDNA collibraries in an expression system, including cross-species cDNA collibraries to identify homologous sequences in other species. The coll was created to facalitate purification cof the Tm 13.17 protein and to try to enhance the anti-freeze activity of the recombinant protein and to try to enhance the anti-freeze activity of the recombinant protein and to try to enhance the anti-freeze activity of the recombinant protein.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cDNA polynucleotide encoding a thermal hysteresis protein which is a Type III anti-freeze protein derived from the Tenebrionoidea Superfamily, useful for providing antifreeze protection to improve the quality of food -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a cDNA polynucleotide comprising sequence encoding a thermal hysteresis protein (THP) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 334; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horwath KL, Myers KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HORW/)
(MYER/)
(EAST/)
                                                    Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-2000; 2000US-210446P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-2001; 2001WO-US18532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIV NEW YORK STATE RES FOUND HORWATH K L.
MYERS K L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EASTON C M.
                               sequence differs from the sequence 13.17 clone/His tag fusion protein.
174 AA,
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and signal peptide"
59..174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Easton
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                                                given in figure 5.11
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Search completed: November 26, 2003, 12:30:21 Job time: 23.1687 secs

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Result
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37
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  SwissProt_41:*
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 Gapext 0
EBYN FUSED
SEDS YEAST
THM ARATH
ARCC HALINI
ERG BUCBP
DCGI YEAST
ECX1 SULTO
TYY1 HUWAN
TYY1 HOWAN
TYY1 MOUSE
YAIS CAEEL
ISH1 SCHPO
KINL LELIM
ROBE
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Q9jlc8
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      baloarcula
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75.7	75.7	75.7	75.7	75.7	75.7	75.7	75.7	75.7	75.7	75.7	75.7
708	704	702	702	691	691	691	672	672	672	899	668
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EFG1_STRCO	EFG CHLTE	EFG YERPE	EFG_THICU	EFG HELPY	EFG HELPJ	EFG CAMJE	VNCS PAVHH	VNCS MUMIV	VNCS MUMIM	VNCS_PAVL3	VNCS_PAVCN
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streptomyce	chlorobium	yersinia pe	thiobacillu	helicobacte	helicobacte	campylobact	hamster par	murine minu	murine minu	parvovirus	canine parv

## ALIGNMENTS

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synthetase.";  Biochemistry (26:8417-8423(1987).  Five Tion:  Five Tion:  A multifunctional enzyme which activates and then thioesterifies adenylated D-2-hydroxylsovaleric acid and a hydrophobic N-methyl-L-amino acid. Peptide bond formation and N-methylation of the amino acid occur before three enzyme-bound dipeptidols are condensed to a hexapeptidol. This then cyclizes	ENZYME REGULATION.  STRAIN=Lambotte et Fautrey; Billich A., Zocher R.; "N-methyltransferase function of the multifunctional enzyme enniatin		AND FUNCTION.  STRAIN=Lambotte et Fautrey;  STRAIN=95324513; PubMed=7601090;  MEDLINE=95324513; PubMed=7601090;  Pieper R., Haese A., Schroeder W., Zocher R.;  Pieper R.;  "Arrangement of catalytic sites in the multifunctional enzyme enniatin synthetase.";  synthetase.";  Fur. T. Becchem. 230,110,136(1985)		SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  STRAIN=Lambotte et Fautrey;  STRAIN=1247491; PubMed=8483420;  MEDLINE=93247491; PubMed=8483420;  Haese A., Schubert M., Herrmann M., Zocher R.;  "Molecular characterization of the enniatin synthetase gene encoding a multifunctional enzyme catalysing N-methyldepsipeptide formation in Fusarium scirpi.";  Fusarium scirpi.";  Mol. Microbiol. 7:905-914(1993).	ESYNI.  ESYNI.  FUBARIUM equiseti (FUBARIUM BCIRPI).  FUBARIUM equiseti (FUBARIUM BCIRPI).  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  NCBI_TaxID=61235;	B-2003 (Rel. 41, Created) B-2003 (Rel. 41, Last sequence updat B-2003 (Rel. 41, Last annotation upc B-2003 (Rel. 41, Last annotation upc tin synthetase [Includes: N-methyloy tin synthetase] tin synthetase [Includes: N-methyloy tin synthetase]	RESULT 1 IDESYN FUSEO STANDARD: PRT: 3131 AA.

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                                                       Query Match
Best Local S
Matches
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InterPro; IPR000873; AMP-bind.
InterPro; IPR0001242; Condensatn.
InterPro; IPR006163; Pp_bind.
InterPro; IPR006162; Ppantne_attach.
InterPro; IPR006162; Ppantne_attach.
IPF00501; AMP-binding; 2.
Pfam; PF00506; Condensation; 2.
Pfam; PF00505; pp-binding; 3.
PFOSITE; PS00075; AMP-BINDING; 2.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 3.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 3.
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HSSP;
GO; GO
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                                                                                                                           MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                          Ligase; Transterase Phosphopantetheine;
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GO:0008168;
GO:0019184;
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SIMILARITY: BELONGS
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                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Methyltransferase; Multifunctional enzyme; pantetheine; Repeat.
          RETVOSTV 600
                          RETIESTV
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BELONGS TO THE ATP-DEPENDENT AMP-BINDING
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by an insertion which cor
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PHOSPHOPANTETHEINE
PHOSPHOPANTETHEINE
PHOSPHOPANTETHEINE
                                                        <u>ب</u>
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Pred. No.
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W; AD7663E91FAB67C4
                                                                                                                                     BINDING
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CARRIER (ACP) 2.
L CARRIER (ACP) 3.
L CARRIER (ACP) 4.
L CARRIER (ACP) 5.
L CARRIER (ACP) 5.
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MEDLINE=97313267; PubMed=9169871;

Johnston M., Hillier L., Riles L., Dubois E., Duesterhoeft A.,

Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,

A. Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,

A. Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,

A. Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

A. Houler-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

A. Mueller-Auer S., Nentwich U., Obermaier B., Rieger M., Rinke M., Rose M.,

A. Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

A. Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

A. Wierendeels F., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

A. Wierendeels F., Voet M., Volkkaert G., Voss H., Wambutt R., Wedler E.,

A. Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1993
01-JUL-1993
15-SEP-2003
                                                                           PROSITE; PS50192; T_SNARE; PROSITE; PS50192; T_SNARE
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288C / AB972;
MEDLINE=97313267; Pub
Johnston M., Hillier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLLINE=93016264; PubMed=1400588;

Hardwick K.G., Pelham H.R.B.;

"SED5 encodes a 39-kD integral membrane protein required vesicular transport between the ER and the Golgi complex.

J. Cell Biol. 119:513-521(1992).
                                                                                                                                                   InterPro; IPR006012; Syntaxin.
InterPro; IPR006011; Syntaxin_N.
InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                      EMBL; X66980; CAA47390.1; -.
EMBL; Z73198; CAA97549.1; -.
                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 387:87-90(1997).
-!- FUNCTION: Required for vesicular transport between the
                                                                                                                                   Pfam; PF00804; Syntaxin;
                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SED5 OR YLR026C
                                                  3D-structure.
                                                                    Coiled coil; Transport;
                                                                                                                                                                                                       30; GO:0005801; C:Golgi cis-face;
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993 (Rel. 26, Last sequence up
993 (Rel. 42, Last annotation
membrane protein SED5.
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                                                                                  SYNTAXIN; 1.
T_SNARE; 1.
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                                                                    Protein transport; Transmembrane;
               CYTOPLASMIC (POTENTIAL).
ANCHOR FOR TYPE IV MEMBRANE
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                      PROTEIN
                                                                      Golgi stack;
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Best Local S
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16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last smotation update)
Thioredoxin M-type-4, chloroplast precursor (TRX AT3G15360 OR MJK13.2.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryoph Spermatophyta; Magnoliophyta; eudicotyledons; coeuroside II; Brassicales; Brassicaceae; Arabidop
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                                                                                                                                                                                                                                                             STRAIN-cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
"RIKEN Arabidopsis full length cDNA clones (RAFLS) seque
SSP consortium (Salk/Stanford/PGEC).";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FACTOR OF A SOA, 864 bp covered by sixty P1 and TAC
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene
EMBL; AF095752; EMBL; AB022218;
                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                            Thie
                                                                                                                                                                       Submitted (MAR-2002) to the EMBL/GenBank/DDBJ database -i- FUNCTION: Participates in various redox reactions reversable oxidation of the active center dithiol.

The M form is known to activate NADP-malate dehydr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mestres-Ortega D., Meyer Y.;
"The Arabidopsis thaliana genome encodes and a new prokaryotic-like thioredoxin.";
Gene 240:307-316(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20047910; PubMed=10580150;
Mestres-Ortega D., Meyer Y.;
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Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THM4
                                                                                                                                                                                                          "Full-length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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nes 6; Conserv
                                                                                 s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                  SUBCELLULAR LOCATION: C
SIMILARITY: BELONGS TO
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85.7%;
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THE THIORED
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Pred. No.
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                                                                                                                                  THIOREDOXIN FAMILY. PLANT M-TYPE
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                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                               (By similarity)
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                                                                                                                                                                      MEDLINE=20504483; PubMed=11016950;
Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski R.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.",
"Genome sequence of Halobacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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CONFLICT
SEQUENCE
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EMBL;
                                                     "Permentative arginine degradation in Halo
(formerly Halobacterium halobium): genes,
transcripts of the arcRACB gene cluster."
J. Bacteriol. 178:4942-4947(1996).
-I- CATALYTIC ACTIVITY: ATP + NH(3) + CO(
                                                                                                                                                                                                                                                                                                                                                                                           Halobacterium sp. (strain Halobacterium salinarium.
                                                                                                                                                                                                                                                                                                                                                                                                                   Carbamate kinase ARCC OR VNG6316G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q48295; Q9HHM9;
01-NOV-1997 (Re
                                                                                                               Ruepp
                                                                                                                                       SPECIES=H.salinarium;
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                                                                                                                                                                                                                                                                                                          STRAIN=NRC-1;
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=64091,
                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                               Plasmid pNRC200
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                                                                                                                            MEDLINE=96326340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006663; Thioredox do InterPro; IPR005746; Thioredoxin.
        SUBCELLULAR SIMILARITY:
                                 phosphate.
PATHWAY: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; AC024081; AAF35402.1;
AF375443; AAK53027.1;
; AY060538; AAL31169.1;
; AY088157; AAM65701.1;
; P80579; 10UM
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PS00194; THIOREDOXIN; 1.
Ive center; Electron transport;
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116
151
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                                Arginine degradation via
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        Belongs
                     LOCATION:
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193
119
151
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35, Last sequence update)
41, Last annotation updat
(EC 2.7.2.2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                            ium; STRAIN=L33;
PubMed=8759859;
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62.5%;
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                     Cytoplasmic
         the
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Pred. No.
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                                arginine deiminase;
                                                       CO(2)
                                                                                                       Halobacterium salinarium
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Best Local S
Matches 6
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MEDLINE=22426901; PubMed=12532265;

Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,

Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,

Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;

"Reductive genome evolution in Buchnera aphidicola.";

"Reductive genome evolution in Buchnera aphidicola.";

Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003)

-i- FUNCTION: This protein promotes the GTP-dependent translocation

-i- FUNCTION: This protein chain from the A-site to the P-site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFG_BUCBP
P59451;
15-SEP-2003
15-SEP-2003
15-SEP-2003
             Complete
NP_BIND
NP_BIND
                                                                             EMBL; AE014017; AAO27176.1; -. HAMAAP; MF 00054; -; 1. PROSITE; PS00301; EFACTOR_GTP;
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2003 (Rel. 42, Last sequence up 15-SEP-2003 (Rel. 42, Last annotation Elongation factor G (EF-G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO0746; arcC; 1.
Transferase; Kinase; Arginine metabolism; Plasmid; Complete SEQUENCE 307 AA; 32534 MW; B8E58C81ED7B8435 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchnera aphidicola (subsp. Baizongia pistaciae).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001048; Aa kinase.
InterPro; IPR003964; Bac_carb_kinase
Pfam; PF00696; aakinase; 1.
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EMBL; X80931; CAA56905.1; -
PIR; T44864; T44864
HSSP; P95474; 1E19.
                                                               Elongation
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                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY
                                                                                                                                                                                                                                                                                    EF-G/EF-2 SUBFAMILY
                                                  lete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                             There are no restrictions ong as its content is in
                                                               GTP-binding
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX."
Nature 387.84-871997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P32460;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEAST
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MEDLINE=92009196; PubMed=1916277;

Yoo H.S., Cooper T.G.;

Yoo H.S., Cooper T.G.;

"Sequences of two adjacent genes, one (DAL2) encoding allantoicase and another (DCG1) sensitive to nitrogen-catabolite repression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCG1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1993
15-SEP-2003
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                                                                                                                                                                                                            ; $4842; $48492.
; $0001469; DCG1.
; $00006807; P:nitrogen
UENCE 244 AA; 27313 M
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OR YIR030C
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27, Last sequence 42, Last annotation
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75.0%;
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85.7%;
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Last annotation update)
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MW; 8B5261745CC0E494 CRC64;
                                                                                                           0
                                                                                                      Pred. No. 42;
0; Mismatches
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Pred. No.
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Matches 5
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P25490; Q14935;
01-MAY-1992 (Rel. 22, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transcriptional repressor protein YY1 (Yin and
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP000982; BAB65433.1; -.
HAMAP; MF 00591; -; 1.
InterPro; IPR001247; 3 EXORNASE.
Pfam; PF01138; RNASE_PH; 1.
Pfam; PF03725; RNASE_PH C; 1.
EXOSOMB; Hydrolase; Nuclease; EXORUCLEASE; Complete proteome.
EXOSOMB; Hydrolase; Nuclease; EXORUCLEASE; Complete proteome.
SEQUENCE 247 AA; 27644 MW; 7EE042B7284C6599 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7."; DNA Res. 8:123-140(2001).
SEQUENCE FROM N.A., AND PARTIAL :
MEDLINE=92005716; PubMed=1655281
                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                 NCBI_TaxID=9606;
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SUBCELLULAR LOCATION: Cytoplasmic
SIMILARITY: BELONGS TO THE RNASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of RNA species (Potential).
SUBUNIT: Component of the archaeal exosome
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5; Conser
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                                                                                                   Primates;
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                       PARTIAL SEQUENCE
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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo K., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Mozley K.C., Hale S., Garcia A.M., Gany L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences."
J. MOI. BIOI. 279:973-986(1998).

-I- FUNCTION: MULTIFUNCTIONAL TRANSCRIPTION FACTOR THAT EXHIBITS POSITIVE AND NEGATIVE CONTROL ON A LARGE NUMBER OF CELLULAR AN VIRAL GENES BY BINDING TO SITES OVERLAPPING THE TRANSCRIPTION START SITE. MAY PLAY AN IMPORTANT ROLE IN DEVELOPMENT AND DIFFERENTIATION. THE FUNCTION OF YY1 AS AN ACTIVATOR OR A REPRESSOR IS SPECIFIED BY THE PRESENCE OF OTHER PROTEINS. FOR EXAMPLE IT ACTS AS A REPRESSOR IN ABSENCE OF ADENOVIRUS EIA PROTEIN BUT AS AN ACTIVATOR IN ITS PRESENCE.
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Park K., Atchison M.;
"Isolation of a candidate repressor/activator, NF-E
that binds to the immunoglobulin kappa 3' enhancer
immunoglobulin heavy-chain mu E1 site.";
n-c Natl. Acad. Sci. U.S.A. 88:9804-9808(1991).
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Cell 67:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-98152931; PubMed-9493912;
McNeil S., Guo B., Stein J.L., Lian J.B., Bushmeyer S., Seto E.,
Atchison M.L., Penman S., van Wijnen A.J., Stein G.S.;
Atchison M.L., Penman S., van Wijnen A.J., Stein G.S.;
"Targeting of the YY1 transcription factor to the nucleolus and the nuclear matrix in situ: the C-terminus is a principal determinant for nuclear trafficking.";
nuclear trafficking.";
J. Cell. Biochem. 68:500-510(1998).
                                                                                                                                                                                                         STRUCTURE BY NMK OF JUJUST 18.0., MEDLINE=98308000; PubMed=9642075; Viles J.H., Patel S.U., Mitchell J.B.O., Uppenbrink J., Doyle P.M., Harris C.J., & Component of a zir
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MEDLINE=97098436; PubMed=8942976;
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MEDLINE=92052179;
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ssion by YY1, a human GLI-Kruppelirelated
repression by adenovirus ElA protein.";
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EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                           , Moody C.M., Justice D.E.,
Sadler P.J., Thornton J.M.;
inc finger with an artificial
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EMBL; M76541; AAA59926.1; -.
EMBL; Z14077; CAA78455.1; -.
EMBL; BC037308; AAH37308.1; -.
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DOMAIN
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Pfam; PF00096; zf-C2H2; 4.
ProDom; PD000003; Znf C2H2; 1.
SMART; SM00355; ZnF C2H2; 4.
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PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0003713; F:transcription co-activator activity; TAS. GO:0003714; F:transcription co-repressor activity; TAS. GO:0003700; F:transcription factority; TAS. GO:0003700; F:zinc ion binding activity; TAS. GO:0008270; F:zinc ion binding activity; TAS. GO:0006960; P:antimicrobial humoral response (sensu Inver. GO:0006357; P:regulation of transcription from Pol II pro. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX. SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A40350; A40350.
1UBD; 23-DEC-96.
1ZNM; 01-APR-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            06357; P:regulation of transcription from IPR007087; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T00915; -
                                                                                                                                                                                                                                                                    196
196
296
301
                                                                                                                                                                                                                                                       371
                                                                                                                                                                                                                                                                                                                                                                regulation; Repressor; Activator; Nuclear protein; Metal-binding; DNA-binding; Repeat; 3D-structure.
43 SP/GLU-RICH (ACIDIC).
                                   ₽,
                                                      397
                                   44712 MW;
      78.4%;
85.7%;
                                                                                                                                                                                                                        INVOLVED IN NUCLEAR MATRIX ASSOCIATION.
INVOLVED IN REPRESSION OF ACTIVATED
TRANSCRIPTION.
INVOLVED IN MASKING TRANSACTIVATION
DOMAIN.
DOMAIN.
H -> R (IN REF. 2).
G -> R (IN REF. 1).
       Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                      C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                   POLY-HIS.
GLY/SER-RICH
                                                                                                                                                                                                                                                                                              C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                          C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                       GLY-RICH.
                                   058C05A0AD2D04E6 CRC64;
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       DB 1;
73;
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                Length 414;
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RESULT
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         EMBL; L13968; AAA40477.1; J
EMBL; L13969; AAA40477.1; J
EMBL; L13965; AAA40477.1; J
EMBL; L13966; AAA40477.1; J
EMBL; L13967; AAA40477.1; J
EMBL; L13967; AAA40477.1; J
                                                                                         EMBL;
                                                                                                                    use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are r
                                                                                                                                                                                                                                                                                                                                                                             Proc.
                                                                                                                                                                                                                                                                                                                                                                                        Hariharan N., Kelley D.E., Perry R.P.;
"Delta, a transcription factor that binds to downst several polymerase II promoters, is a functionally finger protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. PubMed=1309593; MEDILINE=92107191; PubMed=1309593; Flanagan J.R., Becker K.G., Ennist D. Levi B.-Z., Appella E., Ozato K.; "Cloning of a negative transcription upstream conserved region of Moloney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2003 (Rel. 42, Last annotation update) Transcriptional repressor protein YY1 (Yin and yang 1) (YY-1) transcription factor) (NP-E1) (UCR-motif DNA-binding protein) YY1 OR UCRBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E1/UCRBP transcription factor.";
Proc. Natl. Acad. Sci. U.S.A. 90:5559-5563(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Safrany G., Perry R.P.; "Characterization of the mouse gene that encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93296177; PubMed=8516301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92052178;
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                                                                                                                                                                                                                           MURINE LEUKEMIA VIRUS (MULV).
SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                             FUNCTION: MULTIFUNCTIONAL TRANSCRIPTION FACTOR THAT EXHIBITS POSITIVE AND NEGATIVE CONTROL ON A LARGE NUMBER OF CELLULAR AN VIRAL GENES BY BINDING TO SITES OVERLAPPING THE TRANSCRIPTION START SITE. MAY PLAY AN IMPORTANT ROLE IN DEVELOPMENT AND DIFFERENTIATION. THE FUNCTION OF YY1 AS AN ACTIVATOR OR A REPRESSOR IS SPECIFIED BY THE PRESENCE OF OTHER PROTEINS. BIND THE UPSTREAM CONSERVED REGION (UCR) (5'- CGCCATTT-3') OF MOLD THE UPSTREAM CONSERVED REGION (UCR) (5'- CGCCATTT-3')
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                                                 ; AAA40522.1;
; AAA40477.1;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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JR HSSP, P25490; 1UBD.

JR TRANSPAC; T00278; -.

DR TRANSPAC; T00278; -.

DR MGD; MGI:99150; Yy1.

GO; GO:0005667; C:transcription factor complex; IDA.

GO; GO:0003700; P:transcription factor activity; IDA.

DR GO; GO:0003705; P:regulation of transcription, DNA-dependent; IDA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.

DR InterPro; IPR007087; Znf C2H2.

Pfam; PF000096; zf-C2H2; 1.

DR ProDOm; PD000003; znf C2H2; 1.

DR PROSITE; P800026; ZNC_FINGER C2H2_1; 4.

DR Transcription regulation; Repressor; Activator; Nuclear protein;

Zinc-finger; Metal-binding; DNA-binding; Repeat.

Zinc-finger; Metal-binding; DNA-binding; Repeat.

31 CTV-RICH.
RESULT 10

YMIE CAREL

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Best Local S
Matches 6
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15-JUL-1999
15-JUL-1999
16-OCT-2001
                                                                             between the Swiss Institute of Bioinformatics and the Ewn the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.inhibiography.com/
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CONFLICT
SEQUENCE
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ZN FING
  EMBL; U29380
PIR; T27903;
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STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-JCT-2001 (Rel. 40, Last annotation update)
Hypothetical 54.3 kDa protein ZK546.14 in chr
                                                                    or send
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T27903; T27903.
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an email to license@isb-sib.ch).
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85.78;
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Pred. No. 73;
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INVOLVED IN MASKING TRANSACTIVATION
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GLY/SER-RICH
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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gontles M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Motherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Wheller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cruzado L., Usery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RN 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                유
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Best Local S
Matches 5
                                                                stress-responsive nuclear envelope protein. J. Biol. Chem. 277:10562-10572(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | SCHPO | STANDARD; PRT; 684 AA | O9Y77K ( Q09149; | Created) | 28-FEB-2003 (Rel. 41, Last sequence update) | 28-FEB-2003 (Rel. 41, Last annotation update) | 28-FEB-2003 (Rel
                                                                                                                       Taricani L., Tejada M.L., Young P.G.; "The fission yeast ES2 homologue, Bis1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stress response protein ish1.
ISH1 OR ISP1 OR SPBC365.12C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Nuclear protein.
SEQUENCE 472 AA; 54261 MW; 56EA30387545D3DD CRC64;
                                                                                                                                                                                     FUNCTION, SUBUNIT, AND SUBCELLULAR MEDLINE=21895766; PubMed=11751918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BAP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
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Pfam; PF04935; SURF6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Biol. Chem. 277:10562-10572 (2002).
Biol. Chem. 277:10562-10572 (2002).
FUNCTION: Has a role in maintaining cell viability during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 KETVEST 308
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                                                                                                                                                                                                                         AND SUBCELLULAR
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71.4%;
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he EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>۵</u>
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local
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01-NOV-1995
01-NOV-1995
01-OCT-1996
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                      "Molecular characterization of a kinesin-related antigen of Leishmania chagasi that detects specific antibody in African American visceral leishmaniasis.";
Proc. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
-!- DEVELOPMENTAL STAGE: PREDOMINANT IN AMASTIGOTES.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                     STRAIN=MHOM/BR/82 / Isolate BA-2;
MEDLINE=93133867; PubMed=8421715;
                                                                                                                                                                                                                                                                                                                                                                                                                    Kinesin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein. CONFLICT 418
            InterPro;
                        HSSP; P17119; 3KAR
                                      PIR; A47334; A47334.
                                                   EMBL; L07879; AAA29254.1;
                                                                                                                                                                                                                                                                           Reed S.G.;
                                                                                                                                                                                                                                                                                       Burns J.M. Jr., Shreffler W.G., Benson D.R.,
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINL LEICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                         seishmania chagasi.
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SUBCELLULAR LOCATION: Nuclear envelope
SIMILARITY: BELONGS TO THE LEA TYPE 1
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T40319; T40319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
5; Conserv
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        IPR001752; kinesin_motor
                                                                                                                                                                                                                                                                                                                                                                         Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     684 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 32, Created)

(Rel. 32, Last sequence update)

(Rel. 34, Last annotation updat

protein K39 (Fragment).
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75698 MW;
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62.5%;
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Pred. No. 1.2e+02;
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-> E (IN REF. 1).
884CE69714BC7FAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                            oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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RESULT 13
SACS_MOUSE
ID SACS
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Best Local Similarity
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PROSITE; P800411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; P850067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; P850067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; P850067; KINESIN MOTOR DOMAIN2; 1.

MOTOR DOMAIN 1 399

KINESIN MOTOR (BY SIMILARITY)

DOMAIN 426 >955

COILED COIL (POTENTIAL).

NP BIND 122 129

ATP (POTENTIAL).

NP BIND 122 129

7 X 39 AA APPROXIMATE TANDEM
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Q9JLC8;
16-OCT-2001
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REPEAT
NON_TER
         Chaperone.
DOMAIN
DOMAIN
                                           PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                   Engert J.C., Berube P., Mercier J., Dore C., Lepage P., (Bouchard J.-P., Mathieu J., Melancon S.B., Schalling M., Morgan K., Hudson T.J., Richter A.; "ARSACS, a spastic ataxia common in northeastern Quebec, mutations in a new gene encoding an 11.5-kb ORF."; Nat. Genet. 24:120-125(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                 SACS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
REPEAT
                                                                                       EMBL; AF193557; AAF31263.1; -. MGD; MGI:1354724; Sacs.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sacsin.
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                                                                                                                                                                                                                                                                                                                       MEDLINE=20120709; PubMed=10655055;
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090,
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                             L5-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                          L6-OCT-2001
                                                                            MGI:1354724; Sacs.
rPro; IPR001623; Dn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RETIESTV 8
                                            PS50076; DNAJ_1;
PS50076; DNAJ_2;
PS50910; HEPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                           (Mouse)
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75.0%;
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Pred. No.
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Similarity 5; Conserv

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InterPro; IPR001047; Ribosomal S8E.
Pfam; PF01201; Ribosomal S8E; I.
ProDom; PD005658; Ribosomal S8E; 1.
TIGRPAMS; TIGR00307; S8E; 1.
PROSITE; PS01193; RIBOSOMAL S8E; 1.
Ribosomal protein.
SEQUENCE 123 AA; 13549 MW; FB7DB0
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P49402;
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01-NOV-1997
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                      SEQUENCE FROM N.A.

MEDLINE=96127529; PubMed=8590279;

MEDLINE=96127529; PubMed=8590279;

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,

Sugiura M., Tabata S.;

"Sequence analyais of the genome of the unicellular cyanobacterium

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DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein slr0232. sLR0232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE-95391073; PubMed-7662106;
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Archaea, Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Haloarcula.
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                                                                                                                                                                                                                                                                 Synechocystis sp. (strain PCC 6803).
Bacteria, Cyanobacteria; Chroococcales;
NCBI_TaxID=1148;
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J. Protein Chem. 14:189-195(1995).

-i- MASS SPECTROMETRY: MW=11352.4;

-i- SIMILARITY: BELONGS TO THE 88E
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
al protein S8e (HS23).
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Matches 5; Conserv
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PIR; 876385; 876385.
InterPro; IPR000252; DedA.
Pfam; PF00597; DedA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 218 AA; 23781 MW; C04B5D7B7EA7F863 CRC64;
                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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C;Superfamily: acetate-CoA ligase homology; acyl carrier protein homology
C;Superfamily: acetate-CoA ligase homology cacily
F;531-985/Domain: acetate-CoA ligase homology cacily
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                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 2029-2048;430-437;1011-1020;1021-1034;1677-1695;2294-2299 <PIE>
A;Experimental source: strain ETH 1536/J5
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Genetics:

Query Match

593

RETVQSTV 600

1 RETIESTV 8

9 Similarity

Conservative

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89.2%; 75.0%;

Score 33; DB 2; Pred. No. 1.8e+0; Mismatches

.8e+02; 0;

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Gaps

0

Length 3131; Indels

(covalent)

#statue

predicted

A; ACCESSION: 030706 A; Status: nucleic acid sequence not shown A; Molecule type: DNA A; Residues: 499-1074;1572-1988;2423-2566 < A; Cross-references: EMBL: Z18755 A; Experimental source: strain ETH 1536/J5 A; Experimental source: strain ETH 1536/J5 A; Pieper, R.; Haese, A.; Schroeder, W.; Zo Eur. J. Biochem. 230, 119-126, 1995 A; Title: Arrangement of catalytic sites in A; Reference number: 865363; MUID: 95324513; A; Accession: 865363	enniatin synthetase - fungus (Fusarium scir C;Species: Fusarium scirpi C;Date: 31-Dec-1993 #sequence_revision 02-J C;Accession: S39842; S35906; S65363 R;Haese, A. submitted to the EMBL Data Library, Novembe A;Reference number: S39842 A;Accession: S39842 A;Accession: S39842 A;Accession: S39842 A;Coss-references: EMBL:218755; NID:92729; A;Cross-references: EMBL:218755; NID:	RESULT 443
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<pre>/n 5 <ha2> 75 Zocher, R. in the multifunctional enzyme 13; PMID:7601090</ha2></pre>	94 #text_change 03-N 2 :CAA79245.1; PID:g27 R. tin synthetase gene	hypothetical prote hypothetical prote hypothetical prote beta-casein precur oxidoreductase [im vanH protein - Ent hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote citrate synthase - dihydroorotase [im NADH2 dehydrogenas hypothetical prote
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K;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Raccession: A69099

A;Raccession: A69000; MUID:98037514; PMID:9371463
                             RESULT 4
AI0473
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A;Title: SED5 encodes a 39-kD integral membrane protein required for ve A;Accession: A44019
A;Reference number: A44019; MUID:93016264; PMID:1400588
A;Accession: A44019
A;Molecule type: DNA
A;Residues: 1-340 <HAR>
A;Cross-references: EMBL:X66980; NID:94455; PIDN:CAA47390.1; PID:94456
A;Cross-references: EMBL:X66980; NID:94455; PIDN:CAA47390.1; PID:94456
A;Note: sequence extracted from NCBI backbone (NCBIP:116626)
R;Obermaier, B; Piravandi, B; Rinke, M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 21-Jul-2000 C;Accession: A44019; S64853; S23223 R;Hazdwick, K.G.; Felham, H.R.B.
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N;Alternate names: protein L1742; protein YLR026c
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                      A;Cross-references:
A;Map position: 12R
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A; Residues: 1-281 < MTH>
hypothetical protein YPO3890 [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                             F;323-339/Domain: transmembrane #status predicted
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Best Local Similarity

Matches 6; Conserv
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75.0%;
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Pred. No.
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Pred. No.
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                                                                      A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-632 <SAT>
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A; Residues: 1-69 < KUR>
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                                                    A;Cross-references:
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Best Local
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C;Accession: T06586
R;Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.
submitted to the EMBL Data Library, June 1996
A;Description: Identification of a novel family
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C;Superfamily: carbamate kinase
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Halobacterium galinarum
C;Date: 21-Jan-2000 #sequence_revi
C;Accession: T44864
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C;Date: 02-Nov-2001 #sequer
C;Accession: AIO473
                                                                                                                                                                                            DNA-binding protein PD2 - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision
C;Date: 170586
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                                                                                     A;Reference number: Z15774
A;Accession: T06586
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EMBL: X98740; NID: e995229; PIDN: CAA67292.1; PID: e275185
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probable serine/threonine-specific protein kinase (EC 2.7.1.-) F21P8.20 - A N,Alternate names: protein F21P8.20; protein F7H19.320 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence revision 23-Apr-1999 #text_change 31-Jan-2000 C;Accession: T04830; T05145
                  A;Introns: 112/1; 256/1; 303/1; 347/3; 418/1; 497/2; 548/3 A;Note: F21P8.20; F7H19.320 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein C;Keywords: phosphotransferase; protein kinase
                                                                                                                                                                                                                     A,Experimental source: cultivar Columbia; BAC clone F21P8 R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dikse, W.; submitted to the Protein Sequence Database, July 1998 A;Reference number: Z15399
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung
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A; Accession: T04830
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                                                                                                                                                                                   A, Molecule type: DNA
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A; Residues: 1-650 <BI
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Best Local S
Matches 6
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Best Local &
Matches
                                                                                            Map position: 4
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;Cross-references: EMBL:AL031018
;Experimental source: cultivar Columbia;
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;Reference number: AB2577; MUID:21608550; PMID:11743193
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli probable ABC transporter ybjZ;
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85.7%;
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62.5%;
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Pred. No.
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Pred. No. 1.5e+02;
3; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                      G.; Quigley, F.; Mache, R.; Bancroft, tabase, August 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                   protein kinases; protein kinase, homol
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                                                                                                                                                                                                                                                           Stiekema,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding
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                                                                                                                              RESULT 11
S48492
C;Species: Saccharomyces cerevisiae C;Date: 02-Dec-1994 #sequence revision C;Accession: S48492; S19038 R;Rowley, K. submitted to the EMBL Data Library, Oct
                                                                                        DCG1 protein - yeast (Saccharomyces N;Alternate names: protein YIR030c
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                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-89 <SAU>
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Best Local
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hypothetical protein Y48B6A.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text C;Accession: T27007 R;Wall, M. submitted to the EMBL Data Library, September 1999 A;Reference number: Z20297
                                                                                                                                                                                    R;Saunders, D.; Harris, D.; submitted to the EMBL Data
                                                                                                                                                                                                                           C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision
                                                                                                                                         A; Status: preliminary; translated
                                                                                                                                                                                                                                                        hypothetical protein SCI11.10c - Streptomyces coelicolor
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Best Local S
Matches 6
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                                                                                    Experimental source: strain
                                                        SCOEDB:SCI11.10c
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Similarity 5; Conserv
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 Conservative
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                                                                                    EMBL:AL096849; PIDN:CAB50936.1; GSPDB:GN00070; SCOEDB:SCI11.10c
se: strain A3(2)
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                                                                                                                                                                                 D.; James, K.D.;
ata Library, July
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           78.4%;
71.4%;
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85.7%;
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1; Mismatches
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1999
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cerevisiae)

02-Dec-1994

#text\_change

18-Feb-2000

October

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C;Accession: A84233
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, I; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, I; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; I
A;Title: Genome sequence of Halbacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: A84233
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Gene 104, 55-62, 1991
A;Title: Sequences of two adjacent genes, one (DAL2) encoding allantoi
A;Reference number: JH0442; MUID:92009196; PMID:1916277
A;Accession: S19038
               R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: C81325
                                                                                                                                       probable periplasmic protein Cj1193c [imported] - Campylobacter jejuni (strain C;Species: Campylobacter jejuni (strain C;Species: Campylobacter jejuni (strain C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C;Accession: C81325
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C;Genetica
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A; Residues: 1-126, 'C', 128-244
A; Cross-references: GB: M64719
                                                                                                                                                                                                                                   C81325
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                                                                                                                                                                                                                                                      RESULT 13
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A; Residues: 1-267 <STO>
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A;Status:
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Keywords: transmembrane protein
;221-237/Domain: transmembrane #status predicted <TMM>
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preliminary
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85 . 7%;
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Pred. No.
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th, T.; Connerton, P.; Cronin, A.; Davis, r.; David, N.; S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                               uroporphyrinogen III methylase [imported] - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AF0920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: JC2426; MUID:95100950; PMID:7802655
A;Accession: JC2426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription activator/repressor protein delta/YY1 - African cl N;Alternate names: gene FIII protein G;Species: Xenopus laevis (African clawed frog) C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change C;Accession: JC2426; S42062 R;Pisaneschi, G.; Ceccotti, S.; Falchetti, M.L.; Fiumicino, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-268 <PAR>
A;Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73447.1; PID:g696867
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1193c
                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <PAR>
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A; Title: Characterization of FIII/YY1, a Xenopus la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X77698; NID:g455607; PIDN:CAA54777.1; A;Note: The authors translated the codon TTG for residue 71 as
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A; Residues: 1-373 < PIS>
                                                                                                                    A;Cross-references: GB:AL513382; PIDN:CAD09384.1; PID:g16504502; GSPDB:GN00176
                                                                                                                                                                                                 A; Accession: AF0920
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O8xy82 ralstonia s
O8pt27 methanosarc
O8nsv0 corynebacte
O8f8r6 leptospira
O04697 pisum sattv
O8uke4 agrobacteri
O65465 arabidopsis
O9c588 arabidopsis
O9c588 arabidopsis
O8h183 arabidopsis
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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Gloeckner G., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ACI17073, AAM43560.1;
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EMBL, ACI17073, AAM43560.1;
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InterPro; IPR000198; RhoGAP.
Pfam; PF00620; RhoGAP.
1.
SMART, SM00324, RhoGAP, 1.
SMART, SM00324, RhoGAP, 1.
SMART, SM00324, RhoGAP, 1.
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PRELIMINARY;

PRT; 1026 AA.

OBMMU3;

O1-OCT-2002 (TrEMBLrel. 22, Created)

O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

GTPASE-activator protein for RHO-like GTPASeS.

Dictyostelium discoideum (Slime mold).

Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
  01-JAN-1998 (TrEMBLrel. 05,
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Q338e5 mycobacteri
Q826b5 mus musculu
Q91745 xenopus lae
Q8239 salmonella
Q9dwa6 rat cytomeg
Q8209 neurospora
O61867 caenorhabdi
Q9x1m3 thermotoga
Q9hv04 pseudomonas
Q8bsf0 mus musculu
Q43368 arabidopsis
Q81116 chlamydomon
Q9h1w1 homo sapien
Q9u2p7 caenorhabdi
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(C STRAIN=CO-92 / Biovar Orientalis;

(C STRAIN=CO-92 / Biovar Orientalis;

(C STRAIN=CO-92 / Bubwed=11586360;

MEDLINE=21470413; Pubwed=11586360;

A Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

A Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

A Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

A Baker S., Basham D., Davies R.M., Davis P., Dougan G.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

A Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

A Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

A Stimmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.";

BENEL; AJ414159; CAC93357.1; -
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Best Local S
Matches
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01-WAR-2002 (TrEMBLrel. 20, 1
01-MAR-2002 (TrEMBLrel. 20, I
Hypothetical protein YPO3890.
YPO3890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8ZACO;
01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                             Hypothetical protein; Complete proteome. SEQUENCE 69 AA; 7118 MW; FB7BAB2011D6D2C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Kegdle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7125-7155 (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 281 AA;
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TIGRFAMs; TIGR00722; ttdA_fumA_fumB;
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
MCBI_TaxID=187420;
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01-JUN-2002 (TrEMBLrel. 21
Fumarate hydratase, class
MTH1735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae;
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MEDLINE=98037514; PubMed=9371463;
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                                                      Similarity 6; Conser
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21, Last
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Last annotation update)
                                                                                  Score 30;
Pred. No.
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Pred. No.
                                                            Mismatches
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annotation update)
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                                                                                                                   DB 16;
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                                                      Indels
                                                                                                                                                                                                                                                                                           agent of plague.";
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Matches 6
                                                                                                 SEQUENCE FROM N.A.

STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM
MEDIINE=22120827; PubMed=12125824;

Deppenmeier U., Johann A., Hartsch T., Merkl R.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S
Brueggemann H., Lienard T., Christmann A., Boemec
Bruteggemann H., Lienard T., Christmann A., Boemec
Bhattacharyya A., Lykidis A., Overbeek R., Klenk
Fritz H.-U., Gottschalk G.;
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01-MAR-2002
01-MAR-2002
01-MAR-2003
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SEQUENCE
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BMBL; AL646055; CAD15388.1; "InterPro; IPR006453; Gp16 SPP1.

ITIGR?AWs; TIGR01563; gp16 SPP1; 1.
         EMBL; AE013540; AAM32587.1; -.
InterPro; IPR03439; ABC transporter.
InterPro; IPR03338; DUF214.
Pfam; PF02687; DUF214; 1.
                                                                           "The genome of Methanosarcina mazei: evidence transfer between Bacteria and Archaea.";
                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
ABC transporter, permease p
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Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Ralstoniaceae; Ralstonia.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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                                                               J. Mol. Microbiol.
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108 AA;
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Methanosarcinales;
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Klenk H.-P.,
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Q8F8R6;
01-MAR-2003
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SEQUENCE
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InterPro; IPR001406; PseudoU synth 1.
Pfam; PF01416; PseudoU synth 1; 2.
TIGRPANS; TIGR00071; hIsT trua; 1.
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Pseudouridylate synthase (tRNA psi55) (EC 4.2.1.70)
                                                                                                                                                                                   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL, AE011235; AAN47687.1; -.
Helicase, Hydrolase, Complete proteome.
SEQUENCE 433 AA; 50579 MW; 1CB9364C5C1757
                                                                                                                                                                                                                                                                                                            Ren
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Spirochaetes,
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PCRA1 OR LA0488.
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                     STRAIN=56601 /
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CE 289 AA; 31992
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275 AA;
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85.7%;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spirochaetales; Leptospiraceae; Leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Last sequence update)
, Last annotation update)
pcrA (EC 3.6.1.-).
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Pred. No. 1.5e
1; Mismatches
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Pred. No. 1.6e
1; Mismatches
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1.5e+02;
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1.5e+02;
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databases.
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                                                                                                                                                                                       CRC64;
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                                                                                                                        Length 433;
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SEQUENCE FROM N.A.
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S.,
Qurollo B., Goldman B.S., Cao Y., F
Houmiel K., Gordon J., Vaudin M., J
                                                                                                                                                                                                                                                                                             Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almada N.F. Jr., Woo L. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., W.Z., Romero P., Gordo Raymond C., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8UKE4;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=cv. Alaska; TISSUE=Leaf;
Sato N., Kazuno A.A., Ohta N., Ohshima K.;
Sato N., Kazuno A.A. Ohta N., Ohshima K.;
"Identification of a novel family of DNA-binding proteir hook motifs from pea.";
Submitted (JUNN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
ABC transporter, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding protein PI
Pisum sativum (Garden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21608550; PubMed=11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid AT.
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                                                                                                                                                                                   Science
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5; Conserv
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                                                                                                                                                                                                                                              of the natural genetic engineer Agrobacterium tumefaciens
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Last annotation update)
binding/ATPase protein.
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   , Miller N., Blanchard M.,
Askenazi M., Halling C., Mullin
Iartchouk O., Epp A., Liu F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding proteins with two AT-
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Dolan M.,
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 SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/Geni
-i- SHMILARITY: BELONGS TO THE SER/T
EMBL; AL022347; CAAL8460.1; -.

R EMBL; AL031018; CAA19829.1; -.

R EMBL; AL031018; CAA19829.1; -.

R EMBL; AL161558; CAB79268.1; -.

R InterPro; IPR0007019; Prot kinase.

R InterPro; IPR000719; Prot kinase.
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Best Local S
Matches 6
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Protein kinase - like protein (Protein kinase-like pr
P21P8.20 OR F7H19.320 OR AT4G23130.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magmoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Cielo C.,
                                                                                                                                               Massenet C
Mayer K.F.
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EMBL; AE007888; AAK95349.1; --
InterPro; IPR003593; AAA APPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR003838; DUF214
Pfam; PF00005; ABC_tran; 1.
Pfam; PF02687; DUF214; 1.
InterPro;
                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                        Peters S.A., van Staveren M.,
Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Peters S.A., van S
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Bevan M., Massenet O., Clabault G., Quigley F.,
Mewes H.W., Mayer K., Schueller C.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom, PD000006, ABC transporter;
SMART; SM00382, AAA; 1.
PROSITE, PS00211, ABC TRANSPORTER,
Plasmid; Complete proteome.
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"Genome sequence of the plant pathogen
Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
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.W., Mayer K.F.]
ed (JUL-1998) to
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                                                                                                                                                         M N.A.
Clabault G.,
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   DUF26.
Prot_kinase.
Ser_thr_pkinase.
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85.7%;
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Pred. No. 3.9e
1; Mismatches
                                                                          EMBL/GenBank/DDBJ
THE SER/THR FAMILY
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3.9e+02;
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Sear C., Strub G.,
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OF PROTEIN KINASES
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eudicots; Rosidae;
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RESULT 12
Q8H1S3
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Q9C5S8
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Best Local S
Matches
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Q9C5S8;
Q9C5S8;
Q9C5S8;
Q9C5S8;
C1-JUN-2001 (TrEMBLrel. 17, Crear o1-JUN-2001 (TrEMBLrel. 23, Last o1-MAR-2003 (TrEMBLrel. 23, Last o1-mar-or-like protein kinase 6
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Best Local S
Matches 6
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InterPro; IPR000719; Prot kinase.
InterPro; IPR0007290; Ser thr pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF001657; DUF26; 2.
Pfam; PF00069; Dkinase; 1.
PRINTS; PR00109; TYKKINASE.
PRINTS; PR00109; TYKKINASE.
                                                                  Q8H1S3;
Q8H1S3;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000001; Prot_kinase; 1.
PROSITE; P800107; PROTEIN_KINASE_DOM; 1.
PROSITE; P800108; PROTEIN_KINASE_ST; 1.
PROSITE; P800108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; SEQUENCE 659 AA; 73402 MW; 5FEBB6A06FBC3D96 CRC64;
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Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Prot kinase; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 650 AA; 72246 MW; 40C8AC3BB7C5F629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Du L., Chen Z.;
"Identification of genes encoding :
possible targets of pathogen- and i
binding proteins in Arabidopsis.";
Plant J. 24:837-847(2000)
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Hypothetical
                      01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES EMBL; AF224707; AAK28317.1; -.
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Du L., Chen Z.;
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1; Mismatches
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salicylic acid-induced
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3.9e+02;
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Q9U297;
Q9U297;
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01-MAY-2000 (TrEMBLrel 1
01-MAR-2003 (TrEMBLrel 2
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Q8F3H8;
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Bacteria; Spirochaetes;
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Chemotaxis protein CheA.
CHEA2 OR LA2425.
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01-MAR-2003
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Rosidae,
eurosids II, Brassicaies; Brassicaceae, Arabidopsis.
                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
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   SEQUENCE FROM N.A
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                                                        NCBI_TaxID=6239;
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663 AA; 73759 MW; 488E9C67C5727F63 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update
Myosin heavy chain-like protein.
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Pfam; PF02375; jmjN; 1.
SMART; SM00558; jmjC; 1.
SMART; SM00545; JmjN; 1.
SMART; SM00249; PHD; 2.
PROSITE; PS00190; CYTOCHRO
                                                                                 Submitted (MAR-2001) to the EMBL; AP003450; BAB84612.1; Gramene; Q8RZY7; -. SEQUENCE 1051 AA; 117272
                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                             clone: P0034C09.
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Wormbep; Y48B6A.11; CE22126.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR003347; TF_JmjC.
InterPro; IPR003349; TP_JmjN.
InterPro; IPR001365; Znf_PHD.
                                                                                                                                                                                          NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

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5: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

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Compugen Ltd
Sequence 14, Appl Sequence 12, Appl Sequence 2998, Ap Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 31, Appli Sequence 301, Appli Sequence 308, Appli Sequence 270, Appli Sequence 270, Appli Sequence 37, Appli Sequence 9, Appli Sequence 9, Appli Sequence 151, Appli Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,219
FILING DATE: 22-UUL-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 0575/48962/JPW/JKM
TELECOMMUNICATION INFORMATION:
TELEPHAX: (212) 278-0400
TELEPHAX: (212) 278-0400
TELEPHAX: (212) 278-0400
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TELEPHAX: (2112) 278-0400
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US-08-681-219-14
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Publication No. US20020058607A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Takaaki Sato and Junn Yanagisawa
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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12 US-09-983-966-151
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15 US-10-143-090-151
15 US-09-815-242-1393
10 US-09-815-242-133-9
11 US-09-92-331-9
12 US-10-262-313-9
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16 US-10-262-313-9
17 US-09-92-331-9
18 US-09-92-331-9
19 US-09-759-1308-75
19 US-09-759-1308-75
10 US-09-759-1308-75
10 US-09-759-1308-73
10 US-09-9888-615-64
10 US-09-9815-09-44-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151, App Sequence 7, Appli Sequence 1393, Ap Sequence 14836, Ap Sequence 1484, Appli Sequence 8, Appli Sequence 8, Appli Sequence 9, Appli Sequence 76, Appli Sequence 75, Appli Sequence 77, Appli Sequence 78, Appli Sequence 180, Appli Sequence 112, Appli Sequence 112, Appli Sequence 112, Appli Sequence 112, Appli Sequence 12, Appli Sequence 12, Appli Sequence 64, Appli Sequence 62, Appli Sequence 64, Appli Sequence 62, Appli Sequence 63, Appli Sequence 62, Appli Sequence 63, Appli Sequence 64, Appli Sequence 63, Appli Sequence 63, Appli Sequence 64, Appli Sequence 63, Appli Sequence 63, Appli Sequence 64, Appli Sequence 63, Appli Sequence 63, Appli Sequence 63, Appli Sequence 64, Appli Sequence 63, Appli Sequence 64, Appli Sequence 64, Appli Sequence 63, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 63, Appli Sequence 64, Appli Sequence 64,
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US-10-092-138-12
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APPLICANT: Sato, Taka-Aki
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METOCHEMICAL PROTEIN ARRAY BASED ON
TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
PILE REFERENCE: 65023/JPW/PT
CURRENT APPLICATION NUMBER: US/10/092,138
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
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                                    Matches
                                                                Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                  APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, Junn
ITILE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOMAIN AND USES THEREOF
FILE REPERENCE: 48962-A.PCT-US
CURRENT FILING DATE: 1999-05-17
NUMBER: US/09/230,111C
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 33
                                                                                                                   OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:source:synthesized
                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:source:synthesized
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                      ENGTH: 11
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                                                    Local Similarity
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   1 QNFRTYIVSFV 11
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Pred. No. 0.00044;
                                                  Score 56; DB 12;
Pred. No. 0.00044;
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Pred. No. 0.00044;
                                  Mismatches
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Best Local Similarity
Matches 5; Conserva
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US-09-764-891-2998
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SOFTWARE: FastSEQ for
SEQ ID NO 2
LENGTH: 1624
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APPLICANT: Chen, Hongyun
APPLICANT: Le Bihan, Stephane
APPLICANT: Nathwani, Parimal S.
APPLICANT: Connop, Bruce P.
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Matches
               APPLICANT: DENEFLE, Patrice
APPLICANT: ROSIER-MONTUS, Mat
APPLICANT: PRADES, Catherine
APPLICANT: ARNOULD-REGUIGNE,
APPLICANT: DUVERGER, Nicolas
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                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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les 5; Conserv
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55.6%;
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55.6%;
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Sequence 7, Application US/10005338B Publication No. US20030044895A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2998
LENGTH: 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10090454 Publication No. US20020123106A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Connop, Bruce P.
TITLE OF INVENTION: NOVEL ABCA9 TRANSPORTER AND USES THEREOF
FILE REFERENCE: 100103.405
CURRENT APPLICATION NUMBER: US/10/090,454
CURRENT FILING DATE: 2002-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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                                            Marie-Francoise
Isabelle
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Pred. No. 6.1e+02;
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Pred. No.
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DEAN, Michael

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                 CURRENT FILING DATE: 2002-07-26
FRIOR REPLICATION NUMBER: 09/764,892
FRIOR APPLICATION NUMBER: 09/764,892
FRIOR APPLICATION NUMBER: 60/179,065
FRIOR APPLICATION NUMBER: 60/179,065
FRIOR APPLICATION NUMBER: 60/180,628
FRIOR FILING DATE: 2000-01-31
FRIOR APPLICATION NUMBER: 60/214,886
FRIOR FILING DATE: 2000-02-04
FRIOR APPLICATION NUMBER: 60/214,886
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US-10-205-428-391
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Best Local Similarity
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US-09-764-891-4866
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 4866
                                                                                                                                                                                                                                                                      Sequence 391, Applic
Publication No. US20
GENERAL INFORMATION:
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Publication No. US20030077808A1
GENERAL INFORMATION:
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                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA117C1
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PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: FR 00403440.1
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 217
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CURRENT APPLICATION NUMBER: US/10/005,338B
CURRENT FILING DATE: 2001-12-07
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 31
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TYPE: PRT
ORGANISM: Homo Bapiens
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 15; Length 1624; Pred. No. 6.1e+02;
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RESULT 10
US-10-041-860-208
US-10-041-860-208
; Sequence 208, Application US/1004
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
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US-10-205-428-391
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PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1019
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 391
LENGTH: 31
TYPE: PRT
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SEQ ID NO 13
LENGTH: 126
TYPE: PRT
                                                                                 Query Match
Best Local Similarity
                                                                   Matches
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Best Local (
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PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
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PRIOR FILING DATE: 2000-08-14
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PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/220,963 PRIOR FILING DATE: 2000-07-26
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                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                    ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
28 NFRTYNMNWV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                 2 NFRTYIVSFV 11
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FKTYIVTYL 29
                                                                                                                                                                                                                                                                                                                                         Bezabeh, Binyam
                                                                                                                                                                                                                                                                                                                                                           Gazit, Gadi
Weber, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10041860
                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US20030157109A1
                                                                                   58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; Pred. No.
                                                                                   Score 33;
Pred. No.
                                                                   Mismatches
                                                                                   DB 12; Length 126; 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
                                                                                                                                                                                                                                                                                                                           PDGFD AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 31;
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                                                                 Gaps
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Application US/10041860 b. US20030157109A1

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CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 270
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-270
; Sequence 8, Application US/10005338B; Publication No. US20030044895A1; GENERAL INFORMATION:
; APPLICANT: DENEFLE, Patrice APPLICANT: ROSIER-MONTUS, Marie-Francois; APPLICANT: PRADES, Catherine APPLICANT: AROULD-REGUIGNE, Isabelle APPLICANT: DUVERGER, Nicolas; APPLICANT: ALLIKMETS, Rando
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                                                                                                                                                                                       RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT ; ORGANISM: homo sapiens US-10-041-860-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE, ABGENIX, 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 208
LENGTH: 126
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.9%;
Best Local Similarity 60.0%;
Matches 6; Conservative 3
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX.051A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Weber, Richard
APPLICANT: Bezabbh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                           28 NFRTYNMNWV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 NERTYNMNWV 37
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Gazit, Gadi
Weber, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10041860 o. US20030157109A1
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                        Marie-Francoise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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Pred. No. 99;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 126;
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APPLICANT:

APPLICANT:

Murison, James G. Kumble, Krishanand D.

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US-09-866-050A-635

y Sequence 635, Applicate
publication No. US200:
GENERAL INFORMATION:
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US-10-306-878-9
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                                                                                                                                                                                                                                                                                                                     US-10-306-878-9
                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/10306878
Publication No. US20030175819A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Guo, Bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 8
LENGTH: 1543
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                   Query Match
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TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENE-
TITLE OF INVENTION: CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
FILE REFERENCE: ABCA5, 6, 9, 10
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/263,231
PRIOR FILING DATE: 2001-01-23
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: FR 00403440.1
PRIOR APPLICATION NUMBER: FR 00403440.1
PRIOR APPLICATION NUMBER: FR 00403440.1
PRIOR APPLICATION DATE: 2001-12-07
SOFTWARE: Patentin Ver. 2.1
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: UNSURE
LOCATION: 181
OTHER INFORMATION: Xaa=unknown, may be any amino acid
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 135
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                               Match 57.1%;
Local Similarity 66.7%;
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                                                                                                  Application US/09866050A
                                                                                                                                                                                                                                                    Conservative
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                                                                                     US20030040471A1
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                                                                                                                                                                                                                                                                    Score 32; DB 12;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 15;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                     DB 12; Length 135;
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CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 635
LENGTH: 186
TYPE: PRT
ORGANISM: Rat
US-09-866-050A-635
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US-09-984-245-151
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Best Local Similarity 66.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/984,245
CURRENT FILING DATE: 2001-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NITLE OF INVENTION: Compositions Isolated From Skin Cells ITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/048,135
TILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/050,937
FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/041,277 FILING DATE: 1997-03-21
                                                                                       APPLICATION NUMBER: US 60/048,095
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,131
FILING DATE: 1997-05-30
                                                                                                                                                                                    APPLICATION NUMBER: US 60/048,186
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,069
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,094
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/041,276
FILING DATE: 1997-03-21
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/048,352 FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/048,099 FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/048,187 FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/048,188 FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/042,344
                                         APPLICATION NUMBER: US 60/048,096 FILING DATE: 1997-05-30
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o. US20020165374A1
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CATION NUMBER: US 60/048,355
NG DATE: 1997-05-30
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Pred. No. 2.3e+02;
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PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR APPLICATION NUMBER: US 60/060,862
                                                                                                                                                                                                             SEQ ID NO 151
                                                                     Matches
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 343
                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                             LENGTH: 195
180 ONLRTYVRS 188
                                                                     6,
                                                                                                                                                                                                                                                               LING DATE: 1997-10-02
                                  1 QNFRTYIVS 9
                                                                     Conservative
                                                                                     57.1%;
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                                                                                       Score 32; I
                                                                     Mismatches
                                                               JB 1.,
2.4e+02;
2;
                                                                                                    Length 195;
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Gaps

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Search completed: November 26, 2003, 12:38:39 Job time : 20.8795 secs

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No.
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                    Score
     33333335
3333335
3333335
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

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Match Length DB
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Gapop 10.0 , Gapext 0.5
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     QNFRTYIVSFV 11
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAW50177
ABP25867
ABP81504
ABW02762
AAG42749
AAG55302
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AAG42748
AAG55301
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                                                                            Signal-transducing
Streptococcus pned
Streptococcus pned
S. pneumoniae type
Arabidopsis thalia
Arabidopsis thalia
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Human reproductive Arabidopsis thalia Arabidopsis thalia
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Arabidopsis thalia	295	21	æ		34	_
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t HPV	76	23	9		34	٠.
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papi	AAB98400	22	σ		34	_
n papi]	AAB98392	22	σ		34	_
Arabidopsis thalia	AAG22955	21	0		34	
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Human polypeptide	AA009737	22	$\mathbf{r}$		34	Ŭ
immune/	AAM83573	22	90		ω 4	•
Human immune/haema	AAM87832	22	62		34	~
amoyl-pho	AAR55694	15	2391	Ŋ	35	_
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TRICH-30 g	AAE21186	23	1585		35	
gg	AAU78283	23	σ		35	_
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## ALIGNMENTS

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RESULT 1
AAW50177
Inhibition of signal transduction - by inhibiting binding between signal-transducing protein and a cytoplasmic protein, for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal-transducing protein carboxy-terminal peptide
                                                                     WPI; 1998-145347/13.
                                                                                                               Sato
                                                                                                                                                                                                                                                 18-JUL-1997;
                                                                                                                                                                                                                                                                                             12-FEB-1998
                                                                                                                                                                                                                                                                                                                                       WO9805347-A1.
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW50177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW50177 standard; peptide; 11
                                                                                                                                                                                                     22-JUL-1996;
                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                             T, Yanagisawa J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                     96US-0681219.
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RESULT 2
ABP25867
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Matches 11
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          streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GZ (Streptococcus pyogenes), comprising one of 5483 sequences (31), given it the specification. The proteins har intibacterial antiinflammatory activity (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
                                                                                                                             Claim 1;
                                                                                                                                                     New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                          27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus; GAS; GBS; grogroup A streptococcus; Strepantiinflammatory; infection;
                                                                                                 The invention
                                                                                                                                                                                                                                                         Telford J,
Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes.
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                                                                                                                                                                                                                                                                                                 CHIRON SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coccus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; streptococcus; Streptococcus pyogenes; antibacterial; lammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                   ABN66498.
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                                                                                                                          Page 3244; 4525pp; English.
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                                                                                              relates to a protein (ABP25413-ABP30895) from group B
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particularly S.
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                                                                  -ABP30895) ITUM JULE
or group A streptococcus/GAS
or group A streptococcus/GAS
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RESULT 3
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                       The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABP81299-ABP81674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or diagnosing S. pneumoniae infection in a subject. The polynucleotides have antibacterial activity and are useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
Sequence
                                                                                                                                                                                 Claim 42; Page 696-699; 1091pp; English
                                                                                                                                                                                                           preventing S.
otitis media,
                                                                                                                                                                                                                                                                  N-PSDB; ABZ42352.
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                                                                                                                                                                                                                                       New Streptococcus pneumoniae polynucleotides, useful
                                                                                                                                                                                                                                                                               WPI; 2003-093010/08
                                                                                                                                                                                                                                                                                                           Zagursky RJ,
Wooters JL;
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diagnosis; gene
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18-APR-2001;
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Pred. No.
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Query Match

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                              CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering first and second primers, CC which are the nucleic acid cited above or fragments between nucleotides GC 8-100 of a sequence not defined in the specification, for amplifying a CC target sequence contained within a Streptococcus nucleic acid sequence. CC where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers GC having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound CC with the protein, and determining whether the test compound binds to the protein, and determining whether the test compound binds to the contest and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, cc medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, othis media or ear infection. They are also useful in developing of identifiers, and antibiotics. The methods are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection -
                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 4682; 56pp; English.
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the 2469 pro
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  diagnostics and antibiotics. The methods are useful for ng immunodominant proteins. The present sequence is one opposed by the identified coding regions from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  respiratory;
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Note: The sequence data for this patent did not of the printed specification, but was obtained i format directly from WIPO at
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06-MAY-1999
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45.5%;
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promoter; pathway;

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PR 01-JUN-1999; 99US-0137222. PR 03-JUN-1999; 99US-0137528. PR 04-JUN-1999; 99US-0137502. PR 07-JUN-1999; 99US-0137724. PR 08-JUN-1999; 99US-0138094. PR 10-JUN-1999; 99US-0138540.	21-MAY-1999; 24-MAY-1999; 25-MAY-1999; 27-MAY-1999; 28-MAY-1999;	14-MAY-1999; 19-MAY-1999; 20-MAY-1999;	14-MAY-1999; 14-MAY-1999; 14-MAY-1999;	06-MAY-1999; 06-MAY-1999; 07-MAY-1999; 11-MAY-1999;	30-APR-1999; 30-APR-1999; 04-MAY-1999; 05-MAY-1999;	23-APR-1999; 23-APR-1999; 28-APR-1999;	16-APR-1999; 19-APR-1999; 21-APR-1999;	06-APR-1999; 99US-0 08-APR-1999; 99US-0	25-MAR-1999; 99US-012626 29-MAR-1999; 99US-012678	05-MAR-1999; 99US-012318 09-MAR-1999; 99US-012354 23-MAR-1999; 99US-012578	25-FEB-1999; 99US-012	06-SEP-2000.	AA PN EP1033405-A2. XX	OS Arabidopsis thaliana.	<ul> <li>Frotein identification; signal transduction pathway; metabolic pathway;</li> <li>hybridisation assay; genetic mapping; gene expression control; promoter;</li> <li>termination sequence.</li> </ul>	DE. Arabidopsis thaliana protein fragment SEQ ID NO: 70887. XX	DT 18-OCT-2000 (first entry)	AC AAG55302;	AAG55302 ID AAG55302 standard; Protein; 142 AA. YY	RESULT 6	Db 23 QNLSTFIVSF 32	Oy 1 QNFRTYIVSF 10	0.0%; Pred. ve 1; Mi	1tch 64.3%; Sco
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20-AUG-1999;
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l-SEP-1999;
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                                                          Similarity 7; Conserv
QNFRTYIVSF
                                                              Conservative
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70.0%;
                                                            Score 36; DB
Pred. No. 41;
1; Mismatches
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41;
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AAM94340
ID AAM9
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                 26-JUL-2000

26-JUL-2000

14-AUG-2000

12-AUG-2000

12-AUG-2000

12-AUG-2000

13-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

15-AUG-2000

16-SEP-2000

16-SEP-2000

16-SEP-2000

16-SEP-2000

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16-SEP-2000

16-SEP-2000

10-SEP-2000

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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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  2000US-0205113

2000US-0205467

2000US-0214886

2000US-0214886

2000US-0211487

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2000US-0211487

2000US-021963

2000US-0229513

2000US-0225211

2000US-0225211

2000US-0225214

2000US-0225267

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2000US-0184564.
2000US-0186350.
2000US-0189874.
2000US-0190076.
2000US-0198123.
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08-SEP-2000; 08-SEP-2000; 12-SEP-2000;

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RESULT 8
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       PRESERVATION OF A CONTRACT OF 
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                     25-FEB-1999
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06-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 2998; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-465570/50.
N-PSDB; AAL00310.
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2000US-0251859

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2001US-0259678
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99US-0121825
99US-0123180
99US-0123548
99US-0125788
99US-01267864
99US-0126786
99US-0127462
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9966326641956699988665466029326664199153662224888661	041000440010C0010C0400000

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RESULT 9
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ID AAG5301
AAG5
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106 QNLSTFIVSF
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70.0%;
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Pred. No.
1; Mismatc
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RESULT 10

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106 QNLSTFIVSF 115
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9908-0126768.
9908-01267785.
9908-0127462.
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9908-0129845.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
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99US-0161361.
99US-0161992.
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02-AUG-1999 02-AUG-1999 02-AUG-1999 03-AUG-1999 04-AUG-1999 04-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 06-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999

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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                     WPI; 200
N-PSDB;
                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more gennes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ6176-ABLJ611), expressed DNA sequences (ABLJ6175) and the encoded proteins
                                                                                                                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and interactions -
                                                                                       Sequence
                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                              sequences (ABL01840 (ABB57737-ABB72072)
                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 12054; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                       Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB61754;
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DB; ABL05857.
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7; Conserva
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                                                                                       386 AA;
                                             Conservative
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2000US-0614150.
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99US-0161920.
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Pred.
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                                             Mismatches
                                                      No.
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1.2e+02;
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99US-0161406
99US-0161369
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30-AUG-1999; 31-AUG-1999; 01-SEP-1999; 07-SEP-1999; 10-SEP-1999;

18-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 23-AUG-1999 23-AUG-1999 25-AUG-1999 25-AUG-1999 27-AUG-1999 27-AUG-1999

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RESULT 14
ABP81234
ID ABP81
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Best Local S
Matches 6
WO200281695-A2
                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                        Arabidopsis thaliana protein
                                                                                                                          ABP81234;
                                                                                                                                                 ABP81234 standard;
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tietjen K, Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herbicidally active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB92124 standard; Protein;
                         Arabidopsis thaliana
                                                 Posttranscriptional
                                                                                                  27-FEB-2003
                                                                                                                                                                                                                                                                                                                                       useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1335;
                                                                                                                                                                                                               FRAYIINFV 11
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                                                                                                                                                                                                                                                                         66.7%;
                                                 silencing; PTGS; plant; transformation
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                                                                        #62 modulated by PTGS
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1.6e+02;
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non-plant
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RESULT 15
ABB81581
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Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated polynucleic acid segment modulated within a cell by posttranscriptional gene silencing (PTGS). The invention specifically relates to a method to identify an expression product that is modulated by PTGS. The polynucleotide is useful for modulating the gene expression within a cell by PTGS, by introducing the polynucleic acid into a cell and expressing the nucleic acid segment in the cell to form a product. The polynucleic acid segment is also useful for augmenting a cell genome, and for augmenting a plant genome, by contacting a plant cell with the segment to produce a transformed plant cell, and growing the transformed plant cell to produce a differentiated transformed plant. The sequences shown in ABBB1173 - ABBB1298 represent the product of a segment of A. thaliana cDNA modulated by PTGS.
                                                                                                                                                                                                          Human; ABCA5; ABCA6; ABCA9; ABCA10; ATP-binding cassette transporter; chromosome 17; chromosome 17q; chromosome 17q24; antiarteriosclerotic; gene therapy; cholesterol; lipophilic molecule; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleic acid segment useful for within a cell by posttranscriptional gene a plant cell genome -
                                         07-DEC-2000; 2000EP-0403440.
23-JAN-2001; 2001US-263231P.
                                                                                                                                                                                                                                                                     Human
(AVET ) AVENTIS PHARMA SA. (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                  07-DEC-2001; 2001WO-EP15401
                                                                                                                                          WO200246458-A2
                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                             prostaglandin;
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                                                                                                                                                                                                                                                                                                                            ABB81581;
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                                                                                                                                                                                                                                                                  ABC-A-8-1 protein.
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The present invention describes human ATP-binding cassette transporters (CC (ABC). Specifically described are the human ABCA5, ABCA6, ABCA9 and ABCA10 genes (see ABN9594 to ABN9597) which encode the proteins given can ABB81574 to ABB81577). ABN89599 to ABN89715 represent ABCA5, ABCA6, CC ABCA10 genes (see ABN89597). ABN89715 represent ABCA5, ABCA6, ABCA9 and ABCA10 nucleotide fragments; and ABN89716 to ABN89806 represent comparison of the present invention. The ABC sequences have careful for ABCA5, ABCA9 and ABCA10 genes which are used in the case the present invention. The ABC sequences have comparison of the present invention. The ABC sequences have can be used in the manufacture of a medicament intended for the prevention and/or treatment of a subject affected by a dysfunction in the reverse transport of cholesterol. The ABC proteins are involved in the reverse transport of cholesterol. The ABC proteins are involved in the reverse transport of cholesterol. The ABC proteins are involved in the reverse transport of cholesterol, in membrane transport of lipophilic conjecture, in particular inflammation mediating substance such as prostaglandins and prostacyclins, or in any pathology whose candidate conforms and prostacyclins are involved in the manufacture of a medicament intended for prevention of arteriosclerosis in various forms. The ABCA5, ABCA6, ABCA9 and ABCA10 genes are located to chromosome 17, more specifically to the 17q24 locus. Denefle P, Duverger N, A novel nucleic acid corresponding to ATP-binding cassette transporter genes and the encoded polypeptide, useful for preventing or treating a dysfunction in reverse transport of cholesterol -Disclosure; Fig 2; 216pp; English. WPI; 2002-557584/59 Rosier-Montus M, Prad Allikmets R, Dean M; Prades C, Arnould-Reguigne I;

Search completed: November 26, 2003, 12:30:22 Job time: 31.4819 secs 밁 ફ Query Match
Best Local Similarity
Matches 5; Conserv 1077 FMTYVIŚFI 1085 3 FRTYIVSFV 11 Conservative 55.68; Score 36; DB 23; Pred. No. 5.4e+02; Indels 3; Mismatches Length 1580; 0 Gaps

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                                                            InterPro; IPR003593; AAA ATPase.
InterPro; IPR002576; Archaeal ATPase.
Pfâm; PF01637; Archaeal ATPase; 1.
ProDom; PD003808; Archaeal ATPase; 1.
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Hypothetical
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SMART; SM00382; AAA; 1.
SMART; SM00382; AAA; 1.
Hypothetical protein; ATP-binding; Complete proteome.
Hypothetical protein; ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999, PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzderald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F.; Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                EMBL; U67472; AAB98139.1; -. PIR; D64318; D64318.
                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                        Science 275:1489-1490(1997)
                                                                                                                    TIGR; MJ0147;
                                                                                                                                                                                                                                                                          - 1- SIMILARITY: BELONGS TO THE ARCHAEAL ATPASE FAMILY.
                                                                                                                                                                                                                                                                                                                  Koonin E.V.
                                                                                                                                                                                                                                                                                                                              MEDLINE=97197912; PubMed=9045616;
                                                                                                                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                     'Evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2190;
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
LATP-binding protein MJ0147.
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BID HUMAN
Y379 METJA
LOLA COXBU
ATPE BACFI
Y229 ARCFI
MILA BOVIN
ATNB PIG
Y29 WTVN
VP9 WTVN
C1B2 SHEEP
MLIA HUMAN
                088E8FC7D414F8BE CRC64;
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P22476
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P05027
P153027
P153027
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P153027
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methanococc
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01-NOV-1997
01-NOV-1997
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Oleen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstook K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
                                                                                                                                                                                                                                                                               INCETPTO; IPR002576; Archaeal ATPase.
Pfam; PF01637; Archaeal ATPase; 1.
ProDom; PD003808; Archaeal ATPase; 1.
SMART; SM00382; AAA. 1
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                        Hypothetical
NP_BIND
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InterPro; IPR002576;
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TIGR; MJ0801; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Evidence for a family of archaeal ATPases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97197912; PubMed=9045616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Complete genome sequence of the methanogenic archaeon, Methanococcus
|annaschii.":
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29 36
379 AA; 44
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                                                                                                Conservative
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(Rel. 35, Last sequence up
(Rel. 40, Last annotation
ATP-binding protein MJ080
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75.0%;
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75
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6 ATP (POTENTIAL).
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                                                                                                                                                                                                 MW;
                                                                                                Score 38; DB Pred. No. 5.5; 2; Mismatches
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2; Mismatches
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                                                                                                                                                                                                   1BAF2567E0C5D0B4 CRC64;
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MJ0801.
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                                                                                                                                               Length 379;
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RESULT 3
HCM1_YEAST
ID HCM1_YEA
AC P25364;
                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence of the sup61-RAD18 region on Saccharomyces cerevisiae.";
Yeast 8:147-153(1992)
-! FUNCTION: NOT KNOWN
                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1992
01-OCT-1993
15-DEC-1998
                                                                                            DNA BIND
CONFLICT
CONFLICT
                                                                                                                                                                                                                                         SGD; S0000661; HCM1.
GO; GO:000534; C:nucleus; IPI.
GO; GO:0003704; F:specific RNA polymerase II transcription fa.
GO; GO:00077051; P:spindle assembly; IGI.
GO; GO:0007657; P:transcription initiation from Pol II promotes
                                                                                                                                                                                                                                                                                                                           EMBL; L08252; AAA34665.1; -. EMBL; X59720; CAA42280.1; -. PIR; S22262; S22262.
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93180825; PubMed=8441413; Zhu G., Muller E.G.D., Amacher S.L., "A dosage-dependent suppressor of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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HCM1 OR YCR065W OR YCR65W
                                                                                                                               PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00658; FORK HEAD 2; 1.
PROSITE; PS50039; FORK HEAD 3; 1.
DNA-binding; Nuclear protein.
                                                                                                                                                                                            PRINTS; PR00053; FORKHEAD. ProDom; PD000425; TF_Fork_
                                                                                                                                                                                                                  InterPro; IPR001766; TF Fork_head.
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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           Local
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S22262; S22262.
; Q63245; 2HFH.
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l Similarity
7; Conserv
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(Rel.
(Rel.
                                               Ä,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22,
27,
                                                                                                                                                                                          TF_Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNOWN. DOSAGE DEPENDENT SUPPRESSOR
                                                63619
            67.9%;
70.0%;
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Last
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            Score
Pred.
                                                                                  FORK-HEAD.

NV -> KL (IN REF. 2).

TLETQISPRKSSAPDVLTSATNSKFASSGLFGVDVYSVWKR
ATEKISDGNNTTDSNQKHHPYHNHPSNDSGNEKN -> NFG
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                                               (IN REF. 2).
1A9D349F107B91BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
            38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Northrop J.L., Davis T.N.; temperature-sensitive calmodulin the fork head family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain.
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                       DB 1;
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RESULT 4
CHS1_SCHPO
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown D., Brown S., Chillingworth T., Churcher C.M...,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Cillins M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Volckaert G., Aert R., Robben J., Grymonpres B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Caddeu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jinenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RT Mature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                             Bowen A.R., C
Robbins P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHS1 OR SPAC13G6.12C OR SPAC24B11.01C
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01-NOV-1995 (Rel. 32, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Chitin synthase 1 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHS1_SCHPO
P30597;
                                     or send an email to license@isb-sib.ch).
                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92115692; PubMed=1731323;
Bowen A.R., Chen-Wu J.L., Momany M., Young R.,
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 201-389 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                   "Classification of fungal chitin synthases."; Proc. Natl. Acad. Sci. U.S.A. 89:519-523(1992).
                                                                                                                                                                     glucosaminyl))(N+1).

SUBCELLULAR LOCATION: Plasma membrane-bound.
SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.
                                                      Buropean Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                      c. Natl. Acad. Sci. U.S.A. 89:519-523 (1992).
FUNCTION: PLAYS A MAJOR ROLE IN CELL MALL BIOGENESIS.
CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + {(1.4)-(N-acetyl-beta-D-glucosaminyl)}(N) = UDP + {(1.4)-(N-acetyl-beta-D-
                                                                                                                                 SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
Z54308; CAA91105.1;
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PubMed=1731323;
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30-MAY-2000
28-FEB-2003
                                                                       EMBL; D90917; BAA18766.1; -.
PIR; S76854; S76854.
InterPro; IPR003996; RtxC.
Pfam; PF07794; H1yC; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 147 AA; 16960 MW; 4813A700816A4751 CRC64;
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                                                                                                                                                                                                                                                                                          "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                             Kanako T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
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InterPro; IPR001173; Glyco trans 2.
Pfam; PF01644; Chitin synth; 1.
ProDom; PD002998; Chitin synth; 1.
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EMBL; M82957; AAA35297.1;
PIR; S62441; S62441.
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                         7; Conserv
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Pred. No. 19;
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MEDLINE=20021845; PubMed=10553074;
Dascher C.C., Hiromatsu K., Naylor J.W., Brauer P.P., Brown Storey J.R., Behar S.M., Kawasaki E.S., Porcelli S.A., Brenn LeClair K.P.;
                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Conservation of a CD1 multigene family in the guinea pig.";
J. Immunol. 163:5478-5488 (1999).
-i- FUNCTION: NOT KNOWN.
-i- SUBUNIT: ASSOCIATES NON-COVALENTLY WITH BETA-2-MICROGLOBULIN
                                                                                                                                                                                                                                Glycoprotein; Signal; Multigene family.
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Eutheria;
NCBI_TaxID=10141;
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Eukaryota; Metazoa; Chordata;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD1b3 precursor (
                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
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37259 MW;
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CYTOPLASMIC (POTENTIAL).

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Hystricognathi; Caviidae; Cavia.
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EMBL; AB000485; AAC77089.1; --
EMBL; AB0005645; AAC57327.1; --
EMBL; AP002569; BAB38533.1; --
EMBL; AP002569; BAB38533.1; --
ETR; C86108; C86108.
PTR; F91267; F91267.
PTR; S56357; S56357.
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

MITTALE T., Ishii K., Yokoya

Tida T., Tahami H., Honda T., Sasakawa C., Ogasawara N., Yasunaa

Kuhara S., Shiba T., Hattori M., Shinagawa H.,

"Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., Welch R.A., Blattner F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yjdk.
YJDK OR B4128 OR Z5730 OR ECS5110.
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Hypothetical protein; Complete
SEQUENCE 98 AA; 11468 MW; 8
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P39275;
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MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:529-533(2001).
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Tobe T.,
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE014086; AAM67674.1; -.
InterPro; IPR001783; Lum_binding.
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Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson
"50 million years of genomic stasis in endosymbiotic bac
Science 296:2376-2379(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riboflavin synthase alpha chain (EC 2.5.1.9).
RIBE OR BUSG104.
Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RISA_
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                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00677; Lum_binding; 2.
ProDom; PD004110; Lum_binding; 1.
TIGRPAMs; TIGR00187; TibE; 1.
PROSTIE; PS00693; LUM_BINDING; 1.
Riboflavin biosynthesIs; Transferase; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Buchnera.
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REPEAT
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                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: RiboElavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribity1-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethy1-8-lumazine. The alpha subunit catalyzes the dismutation of 6,7-dimethy1-8-lumazine to riboflavin and 5-amino-6-(1'-D)-ribity1-amino-2,4(1H,3H)-pyrimidinedione (By similarity).

CATALYTIC ACTIVITY: 2 6,7-dimethy1-8-(1-D-ribity1)lumazine = riboflavin + 4(1-D-ribity1amino)-5-amino-2,6-dihydroxypyrimidine.

PATHWAY: Pinal steps of riboflavin synthesis.

SUBUNIT: Oligomer that consist of 3 alpha subunits and 60 beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUXL (LUMP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO BIOLUMINESCENCE ANTENNA PROTEINS
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                                                                                                                                                                                                               Similarity 60. 6; Conservative
                                                                                                                                                  KNFHTYTVNF
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81
179
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(Rel. 41, Last annotation update)
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60.0%;
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Pred. No. 11;
2; Mismatches
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INDS TO LUMAZINE (PROBABLE)
CE00EE91A2C732AF CRC64;
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ersson S.G.E.;
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RA Kunst F. Ogasawara N. Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Brom S.,
RA Browillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Gimm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gimm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konlingstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Railly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parco V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Skiyuchi J., Sekowaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).

1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.

1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome subtilis.";
EMBL; Z28592; CAA82254.1; -.
EMBL; Z99122; CAB15704.1; -.
PIR; I40362; I40362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
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J. Bacteriol. 176:6802-6811(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol.
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Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                           H(+) (Out).
SUBUNIT: F-TYPE.ATPASES HAVE 2 COMPONENTS, CF(1).
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CI
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), 1
HAS THREE MAIN SUBUNITS: A, B AND C.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. (
POTENTIAL TRANSMEMBRANE DOWAINS.
SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                 a collaboration -
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28-FEB-2003
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InterPro; IPR000568; ATPSynt Asub.

Pfam; PF00119; ATP-Synt A; 1.

PRINTS; PR00123; ATPASEÄ.

TIGRRAMS; TIGR01131; ATP synt 6 or A; 1.

PROSITE; PS00449; ATPASEÄ, 1.

PROSITE; PS00449; ATPASEÄ, 1.

Hydrogen ion transport; CF(0); Transmembrane; Complete proteome.

SEQUENCE 244 AA; 27054 MW; E26172BA9F1AA248 CRC64;
                                                                                                              PRINTS; PR00123; ATPASEA.

TIGRPAMs; TIGR0113; ATP synt 6 or A; 1.

PROSITE; PS00449; ATPASEA; 1.

Hydrogen ion transport; CF(0); Transmembrane.

SEQUENCE 261 AA; 28982 MW; 83E887398D608E
                                                                                                                                                                                                                                                                                                                          EMBL; X05302; CAA28923.1; -. PIR; S10826; PWYCA6. HSSP; P00855; 1C17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cozens A.L., Walker J.E.;
"The organization and sequence of the genes for ATP synthase subunits in the cyanobacterium Synechococcus 6301. Support for an endosymbiotic origin of chloroplasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase A chain (EC 3.6.3.14) (Protein 6).
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MEDLINE=87311713; Pubmed=3041005;
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                                                                                                                                                                                                                                                                  Pfam; PF00119; ATP-synt_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                              nterPro; IPR000568; ATPsynt_Asub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALY CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIV SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). HAS THREE MAIN SUBUNITS: A, B AND C.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 8 POTENTIAL TRANSMEMBRANE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MO. Biol. 194:359-383(1987).

NOTICE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.

CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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Similarity 5; Conserv
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                        62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chroococcales; Synechococcus.
                        Score 35;
Pred. No.
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                                                                                                                     83E887398D608E8C CRC64;
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                                                       DB 1; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 244;
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RESULT 12
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AC Q9ZCG1
AC Q0ZCG1
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AC Q0
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Best Local S
Matches 5
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Q9ZCG1;
28-FEB-2003
28-FEB-2003
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Q36428;
                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
NADH-quinone oxidoreductase chain L (EC 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00361; oxidored_q1; 1.
Pfam; PF00662; oxidored_q1 N;
PRINTS; PR01434; NADHDHGNASE5.
Oxidoreductase; NAD; Ubiquinon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MBL; X80245; LANDULL DATE OXTED STREET OXIDATE OXTED STREET OXIDATE OX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
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Mol. Byol. 41:928-941(1995).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
SEQUENCE FROM STRAIN=Madrid
                                                                                                                                                                                                                  Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96139026; PubMed=8587138;
MEDLINE=96139026; PubMed=8587138;
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Neoptera; Orthopteroidea; Orthoptera; Caellfera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        īs-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                                                               Rickettsiaceae; Rickettsieae;
                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                                                                                                                                                                                        NUOL OR RP792.
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                                                                                                 NCBI_TaxID=782;
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                                                                                                                                                                                                                                                                                      chain L) (NDH-1,
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Pred. No.
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                                                                                                                                                  Rickettsia
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(EC 1.6.99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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Matches &
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PFANN'S; PR01434; NADHDHGNASES.
Oxidoreductase; NAD; Quinone TRANSMEM
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
NADH-quinone oxidoreductase chain L (EC 1.6.99.5) (NADH dehydrogenase I, Chain L) (NDH-1, Chain L).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondria.";
Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003916; NADHub oxred5.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicharitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Briksson A.-S., Winkler H.H., Kurland C.G., "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andersson S.G.E.
Sicheritz-Ponten
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CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
SUBCELLULAR IOCATION: Integral membrane protein (Potential).
SIMILARITY: TO POLYPEPTIDE 5 OF THE NADH-UBIQUINOL OXIDOREDUCTASE OF CHLOROPLASTS OR MITOCHONDRIA.
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                                                                                                                                                                                                6; Conserv
                                                                                                                                                   NYTLYIVSFI 640
                                                                                                                                                                         NFRTYIVSFV
                                                                                                                                                                                                 Conservative
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                                                                                       STANDARD;
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                                                                                                                                                                                                                                                  73477
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                                                                                                                                                                                                            Score 35;
Pred. No.
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540436E913D097B4 CRC64;
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                                                                                       657
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InterPro; IPR0013916; NADHub_oxred5.
InterPro; IPR001759; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1_N.
Pfam; PF00361; oxidored_q1_N; 1.
Pfam; PF00363; oxidored_q1_N; 1.
PRINTS; PR01434; NADHDHGNASE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01434 Oxidoreductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 293:2093-2098(2001).
-I- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogata H., Audic S., Samson D., Roux V., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21442074; PubMed=11557893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfur (Fe-S) centers, to quinones in the respiratory chain.

Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient (By similarity).

CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.

SUBCELLULAR LOCATION: Integral membrane protein (Potential).

SIMILARITY: TO POLYBEPTIDE 5 OF THE NADH-UBIQUINOL OXIDOREDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF CHLOROPLASTS OR MITOCHONDRIA.
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                                                                                                    73327
                                                              62.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in Rickettsia conorii and R.
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Pred. No. 36;
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                                                  <u>.</u>.
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RESULT 14
ATPI GALSU STANDARD;
ID ATPI GALSU STANDARD;
AC P35008;
DT 01-FEB-1994 (Rel. 28, Created)

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ATPI OENHO
ID ATPI OENHO
AC O9MTMO;
DT 15-SEP-2003
DT 15-SEP-2003
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15-SEP-2003 ()
ATP synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOSTIZEWA M., Zetsche K.;
"Organization of plastid-encoded ATPase genes and flanking regions including homologues of infB and tsf in the thermophilic red alga faldieria sulphuraria.";
Plant Mol. Biol. 23:67-76(1993).
-i- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBERANI OF THE CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                             SEQUENCE
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Chloroplast.
               ATPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
Oenothera hookeri (Hooker's evening primrose)
                         ATP synthase
                                                                                                                                                                                                                                                                                                                                                          Hydrogen ion
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00119; ATP-synt_A; PRINTS; PR00123; ATPASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X67814; CAA48020.1; -. HSSP; P00855; 1C17.
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STRAIN=14-1-1 / Isolate 107.79/Goettingen;
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                                                                                                                                                                                                                      Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thylakoid membrane.
SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
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ion transport; CF(0);
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A chain precursor (EC 3.6.3.14)
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(Rel. 42, Last annotation
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211
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                           A chain
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PRINTS; PR00123; ATPASER.

TIGRAM; TIGRO1131; AIP-Synt_6_or_A; 1.

PROSITE; PS00449; ATPASE A; 1.

PROSITE; PS00449; ATPASE A; 1.

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Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Myrtales; Onagraceae; Oenothera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comment entitles requires a license agreement (See http://www.isb-sib.ch/annot or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thylakoid membrane.
-I- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIRECT ROLE IN THE TRANSLOCATION OF PROTONS A -I - CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20309318; PubMed=10852478;
Hupfer H., Swiatek M., Hornung S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eurosids II; Myrt
NCBI_TaxID=85636;
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Pfam; PF00119; ATP-synt_A; 1.
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    -!- SUBCELLULAR LOCATION: Integral membrane protein.

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of the five distinguishable
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edons; core eudicots; Rosidae;
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58.9	58.9	58.9	59.8	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7
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## ALIGNMENTS

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C;Genetics:
A;Gene: all3271
C;Superfamily:
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                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-372 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74970.1; PID:g17132366; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                          Nakazaki, N., Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anna, Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein all3271 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2214
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, M.; Tabata, E.
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A;Molecule type: DNA
A;Residues: 1-250 <PAR>
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;Experimental source: serotype O2, strain NCTC 11168
      Query Match
                                                                                                   all3271
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                                                                hypothetical protein yxaB
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72.7%;
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cobyric acid synthase CbiP [imported] -
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Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Accession: A64400
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blai; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
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A;Cross-references: GB:U67524; GB:L77117; NID:g2826321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein MJ0147 - Metha
C;Species: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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/Species: Methanococcus jannaschii
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ATP-binding prote
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1; Mismatches
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odek, A.
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    Superfamily: unassigned fork head proteins; fork head DNA-binding;
Keywords: DNA binding; nucleus;
109-198/Domain: fork head DNA-binding domain homology <FHD>
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A;Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42280.1; PID:g1907205; MIPS:1 R;Zhu, G.; Muller, E.G.; Amacher, S.L.; Northrop, J.L.; Davis, T.N. Mol. Cell. Biol. 13, 1779-1787, 193
A;Title: A dosage-dependent suppressor of a temperature-sensitive calmodulin mutant A;Reference number: A48153; MUID:93180825; PMID:8441413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:X59720; EMBL:S93798; NID:g1907116; PIDN:CAA42280.1; PID:g1907205 R;Antoine, G.; Benit, P.; Chanet, R.; Fabre, R.; Faye, G.; Fukuhara, H.; Mathieu, A.; So submitted to the Protein Sequence Database, March 1992
A;Reference number: S19477
                            A;Cross-references: SGD:S0000661; MIPS:YCR065wA;Map position: 3R
                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-128,'NV',131-489,'TLETQISPRKSSAPDVLTSATNSKFASSGLFGVDVYSVWKRATEKISDGN','NTT
A;Cross-references: EMBL:L08252; NID:g171653; PIDN:AAA34665.1; PID:g171654
                                                                                                                                                                                                                                                                                                                                   A;Note: sequence extracted from NCBI backbone (NCBIN:125990, NCBIP:125991) R;Zhu, G.; Muller, E.G.; Amacher, S.L.; Northrop, J.L.; Davis, T.N. submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-489,'TLETQISPRKSSAPDVLTSATNSKFASSGLFGVDVYSVWKRATEKISDGNNT','TDSNQKHHPYHNHP
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A; Residues: 1-532 < ANT >
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C;Superfamily: probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: C97069
A;Status: preliminary
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C;Date: 14-Sep-2001 #sequence_revisio:
C;Accession: C97069
                                                                                                                                                                                                                                      A; Accession: S30779
                                                                                                                                                                                                                                                                             A; Reference number: S30779
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A; Residues: 1-491 < KUR>
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                                                                                                                      Genetics:
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names: protein YCR065w; protein YCR902
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Pred. No. 14;
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n; rettelln, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heion, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001

A; Aluthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A; Reference number: A95000; MUID:21357209; PMID:11463916

A; Status - 7771-1-1
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S62441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chitin synthase (EC 2.4.1.16) CHS1 - fission yeast (Schizosaccharomyces pomb N,Alternate names: protein SPAC1366.12c; protein SPAC24B11.01c C;Species: Schizosaccharomyces pomb C;Species: Schizosaccharomyces pomb C;Date: 16-May-1996 #sequence revision 13-Mar-1997 #text_change 20-Oct-2000 C;Accession: S62441; S62546; C45189; T37647; T38328 R;Odell, C.; Bowman, S.
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A;Molecule type: DNA
A;Residues: 201-272,'R',274-389 <BOW>
A;Residues: 201-272,'R',274-389 <BOW>
A;Residues: 201-272,'R',274-389 <BOW>
A;Residues: 201-272,'R',274-389 <BOW>
A;Rose: Bequence: GB:M82957; NID:g173367; PIDN:AAA35297.1; PID:g173368
A;Note: Bequence extracted from NCBI backbone (NCBIP:75847)
A;Note: Bequence extracted from NCBI backbone (NCBIP:75847)
R;Note: Bequence extracted from NCBI backbone (NCBIP:75847)
A;Note: Bequence extracted from NCBI backbone (NCBIP:75847)
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A;Reference number: A38192; MUID:92115692; PMID:1731323 A;Accession: C45189
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A; Residues: 1-850 < KUR>
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A; Residues: 1-859 < ODE>
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Residues: 1-199 <ODW>
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         Walsh, S.V.; Wood,
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P.J.; Robbins,
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K;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Mio, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 832/2
C;Superfamily: chitin synthase chsA
C;Keywords: glycosyltransferase; he
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A;Residues: 1-199 < DD3-
A;Residues: 1-199 < DD3-
A;Cross-references: EMBL:267757; PIDN:CAA91766.1; GSPDB:GN00066; SPDB:SPAC24B11.01c
A;Experimental source: strain 972h-; cosmid c24B11
C;Genetics:
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A;Accession: T37647
A;Accession: T37647
A;Molecule type: DNA
A;Residues: 1-859 <OD2>
A;Cross-references: EMBL:Z54308; PIDN:CAA91105.1; GSPDB:GN00066; SPDB:SPAC13G6.12c
A;Experimental source: strain 972h-; cosmid c13G6
A;Experimental source: strain 972h-; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21786
A;Accession: T38328
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                                                                                                                                                   A;Cross-references: EMBL:D90917;
A;Note: the nucleotide sequence of C;Superfamily: hemolysin C
                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 17-Feb-2003
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R; Kaneko, T.; Sato,
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A;Gene: CHS1; SPAC24B11.01c;
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                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                               A; Title: Sequence analysis of the genome of
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Yamada, M.; Yas
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hypothetical protein T30F21.21 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001 C;Accession: H96B12 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A;Authors: Hunter, J.L.; Jenkins, J.; Jenkins, J.; Jenkins, J.; Jenkins, J.; Jenkins, J.; Jenkins, Jenk

l, S.; White, Creasy, T.H.;

O.; Alonso; Dewar, K.

Khaykin, Maiti, R

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Marziali Kin, H96812

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R;Murray, J.
submitted to the EMBL Data Library, April 1997
submitted to the sequence of C. elegans cosmid ZC196.
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                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-412 < ALC>
                                                                                                                                                                                                        R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, January 2000 A;Reference number: Z23021 A;Reference number: Z23021 A;Accession: T46104
                                                                                                                                                                                                                                                                                                          hypothetical protein T25B15.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 28-Jul-2000
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                     A; Note: T25B15.110
                                        A; Introns: 20/3;
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A; Residues: 1-225 < STO>
                                                             A; Map position: 3
                                                                                                      A; Experimental source: cultivar Columbia; BAC clone
                                                                                                                           A;Cross-references: EMBL:AL132972
                                                                                                                                                                                                                                                                                           C;Accession: T46104
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A;Experimental source: strain Bristol N2; clone ZC196
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A; Residues: 1-374 < MUR>
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A; Accession: T25943
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Matches 6
                                                                                                                                                                                     Status: preliminary
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Best Local Similarity
Matches 7; Conserv
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                                          155/3; 220/3; 317/1; 369/1; 384/3
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1034 <KUR>
A;Conserreference: GB:AE006469; PIDN:AAK64659.1; PID:g14523056; GSPDB:GN00165
A;Experimental source: Strain 1021, megaplasmid pSymA
A; Abola, P.; Ampe, F.; Barloy-Hubler
R;Galibert, F.; Ampe, F.; Barloy-Hubler
R;Galibert, F.; Comie, A.; Barloy-Hubler
L; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A;Fitle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A; Genome: plasmid
C; Superfamily: formate deh:
C; Keywords: oxidoreductase
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A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: A95262
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A; Residues: 1-510 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.M.; Vente
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable formate dehydrogenase (EC 1.2.1.2) alpha chain FdoG [imported] -
C;Species: Sinorhizobium meliloti
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C; Superfamily: pectinesterase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   멼
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Query Match

64.3%;

Score 36;

DB 2;

Length 1034;

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hypothetical protein C0820w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18489
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18489
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-981 <LAW>
A;Cross-references: EMBL: Z98551; NID:e1331903; PID:e1331910; PIDN:CAB11128.1
C;Genetics:
A;Map position: 3
A;Note: C0820w
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Search completed: November 26, 2003, 12:36:01 Job time: 12.2048 secs
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                             2 NFRTYIVSF 10
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1536 NFQTYITTF 1544
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508 QNYRKFMVSF 517
                                                                                                                                                                         64.3%;
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pred. No. 3.2e+02;
2; Mismatches 1
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Perfect score:
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Maximum DB
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungl:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
9: sp_phage:*
10: sp_plant:*
11: sp_vordent:*
12: sp_virus:*
13: sp_virus:*
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092513; PRELIMINARY;
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STRAIN-E-1;

Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;

Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;

"Complete nucleotide sequence of Staphylococcus aureus E-1 E

plasmid.";

SHOUTHIER OF THE STREET O
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Plasmid EDINA plasmid.
Bacteria; Firmicutes; Bacillales;
NCBI_TaxID=1280;
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Q8r0r4 mus musculu
Q8c0a9 mus musculu
Q8c114 mus musculu
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Q34505 bacillus su
Q97311 plasmodium
Q9lup2 arabidopsis
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01-OCT-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
Major antigenic peptide I
PEB3 OR CJ0289C.
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MEDLINE=98378056; PubMed=9714254;
Moenig R., Pleij C., Beier C., Commandeur U.;
"Genome properties of beet virus Q, a new furo-like sugarbeet, determined from unpurified virus.";
J. Gen. Virol. 79:2027-2036(1998).
EMBL; AJ223597; CAA11459.1; -.
InterPro; IPR001337; TWV coat.
Pfam; PF00721; TWV coat; 1.
Pfam; PF00721; TWV coat; 1.
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae, Campylobacter.
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MEDLINE=20150912; PubMed=10688204;

MEDLINE=20150912; PubMed=10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Parkhill J., Wren B.W., Mungall K., Feltwell T., Holroyd S.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Whitehead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacter jejuni
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Beet virus Q.

Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.

NCBI_TaxID=71972;
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EMBL; AL139074; CAB72756.1; -.
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Q97JB2;
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01-OCT-2001
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"Complete genomic sequence of the filamentous nit:"Complete genomic sequence nit:"Complete genomic sequence nit:"Comple
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                                                                           Clostridium acetobutylicum. Bacteria; Firmicutes; Clost Clostridium.
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"Mechanism of bacteriophage SfII-mediated
Shigella flexneri.";
Mol. Microbiol. 26:939-950(1997).
EMBL; AF021347; AAC39273.1;
SEQUENCE 486 AA; 55778 MW; C9D597EAF3C
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01-DEC-2001
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EMBL; AP003592; BAB74970.1;
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MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P.,
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NCBI_TaxID=103690;
[1]
SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
                                                                                                                                                       Cobyri
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MEDLINE=98086100; PubMed=9426131;
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                                                     NCBI_TaxID=1488;
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372 AA; 43535 MW;
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ima K., Kimura T.,
A., Muraki A.,
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Matches 6
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zer
Noelling J., Breton G., Omelchenko M.V., Hitti J., Wolf Y.I.
Glbson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-pi
bacterium Clostridium acetobutylicum.";
J. Bacteriol 183:4823-4838(2001).
EMBL; AB007649; AAK79342.1; -.
InterPro; IPR000515; BPD_transp.
InterPro; IPR002586; CbiA, P.
InterPro; IPR004459; CobQ.
Pfam, PP01656; CbiA; 1.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical phage protein spyM18_0369 (Hypothetical phage protein SpyM3_0710).
SpyM18_0369 OR SPYM3_0710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8P2G3
Q8P2G3;
emergence.",
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
EMBL; AE00980; AALB9120.1; -.
EMBL; AE014151; AAM79317.1; -.
InterPro; IPR005021; Phage termin.
Pfam; PP03354; Phage_terminase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 576 AA; 67816 MW; 4D64454743347AA3 CRC64;
                                                                                                                                                                                                                                                                                                           SPECIES=S.pyogenes; STRAIN=MGAS8232 / Serotype M18;
MEDLINB=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";
                                                                                                                                       Campbell D.S., Smith T.M., Mcc
Schlievert P.M., Musser J.M.,
Schlievert e.M., Musser J.M.,
"Genome sequence of a serotype
"Genome sequence of a serotype
"Herbidge of the high
                                                                                                                                                                              SPECIES=S.pyogene8; STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., P
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes (serotype M18), Streptococcus pyogenes (serotype M3). Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                "Genome sequence of a serotype M3 strain phage-encoded toxins, the high-virulence
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Pred. No. 38;
3; Mismatches
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Q9N891;
01-OCT-2000
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01-OCT-2002
01-MAR-2003
                                                                         Oliver K., Bowman S., Hall N., Quail M., Rajandream M.A., del Portillo H.A., Lanzer M., Barrell B.G., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL360354; CAB96704.1; SEQUENCE 312 AA; 36805 MW; 2DZAO8FBB4DE0DCA CRC64;
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Eukaryota; Alveolata;
NCBI_TaxID=5855;
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Hypothetical protein.
SEQUENCE 737 AA; &
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Rhabditidae; Peloderinae;
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MEDLINE=99069613; PubMed=9851916;
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l protein ZC581.3.
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01-DEC-2001
01-DEC-2001
01-MAR-2002
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01-MAR-2003
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris B., Lennard N., Clark L., Line A., Barron A., Corton C., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B., Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AL844509; CAD52484.1; -. SEQUENCE 633 AA; 75557 MW; CB3C43CBBFC4D865 CRC64;
                                                                                   "Avian influenza A H5N1 and H9N2 viruses bearing a specific constellation of nonglycoprotein genes caused illness in humans."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF257202; AAK49345.1; -.
InterPro; IPR001009; RNA pol_P2.
Pfam; PF00603; Flu PA; 1.
SEQUENCE 716 AA; 82699 MW; E6F31F77891EE48F CRC64;
                                                                                                                                                                       STRAIN=A/Hong Kong/97/98;
Shaw M.W., Cooper L.A., Xu X., Thompson
Zhou N.N., Kilmov A., Cox N.J., Webster
                                                                                                                                                                                                                                                                                 RNA polymerase
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Viruses; ssRNA negative-strand viruses; Ort
Influenza A viruses; Influenzavirus A.
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NCBI TaxID=36329;
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RESULT 12
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Q915A5;
01-DEC-2001
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Q97N40;
Q1-OCT-2001 (TrEMBLrel. 18,
01-OCT-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                               Submitted (OCT-2001) to the EMBL/GenBank/DDBJ EMBL; AF427517; AALIGO90.1; -. InterPro; IPR007099; RNA pol NSvir. PROSITE; PS50525; RDRP FLU; I. SEQUENCE 2190 AA; 252091 MW; C16DF73E38E58
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AN3/35,
Zhang L., Marriott K.A.,
Zhang L., marriott K.A.,
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Viruses; ssRNA negative-strand
NCBI_TaxID=11630;
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EMBL; AE007510; AAK76279.1;
TIGR; SP2231; -.
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Pred. No. 2.6e+02;
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Matches 5
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PKELATALON
Q9SYN6;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF204951; AAK14454.1; -.
InterPro; IPR001214; SET.
SMART; SM00317; SET; 1.
SMART; SM00317; SET; 1.
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01-JUN-2002
01-JUN-2002
01-MAR-2003
                                                                                                              SEQUENCE FROM N.A.

SHOOKS S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Shinn P., Altafi H., Bei Q., Chin C., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                       STRAINECY. COlumbia;
Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Rederspiel N.A., Palm C.J., Rowley D., Buehler E., Dunn H., Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn B., Gonzalez A., Kremenetekaia I., Kim C., Lenz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A. Ecker J.R.;
Submitted (FEB-200
                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ectocarpus siliculosus virus.
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
NCBI_TaxID-37665;
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                                                               Submitted
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                                                                                          Genomic sequence for Arabidopsis thaliana BAC F3F9 from
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the EMBL/GenBank/DDBJ databases.
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                                                           EMBL/GenBank/DDBJ databases.
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RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E.,
RA Chan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC017260; AAD30590.1; -.
DR EMBL; AC017460; AAD30590.1; -.
DR EMBL; AC01740; AAP71794.1; -.
DR Ffam; PF04832; SOUL; 1.
DR Pfam; PF04832; SOUL; 1.
SQ SEQUENCE 225 AA; 25338 MW; DOCA9754C381471C CRC64;
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Best Local S
Matches 7
106
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QNLSTFIVSF
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Search completed: November 26, 2003, 12:34:32 Job time : 25.988 secs

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Perfect score:
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               Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Gapop 10.0., Gapext
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64
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102.059 Million cell updates/sec
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            GenCore version (c) 1993 - 2003
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        US-08-681-219-15
2 US-10-092-138-13
2 US-09-230-111C-13
5 US-10-101-464A-816
5 US-10-101-464A-975
5 US-10-101-464A-977
2 US-10-032-585-7531
1 US-09-759-130B-196
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Compugen Ltd
Sequence 15, Appl Sequence 13, Appl Sequence 13, Appl Sequence 816, Appl Sequence 905, App Sequence 975, App Sequence 977, App Sequence 196, App Sequence 197, App Sequence 397, App
                                                                                                                                                                                                                                                                               Description
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               US-08-681-219-15
US-08-681-219-15
US-08-681-219-15
Sequence 15, Application US/08681219
Publication No. US20020058607A1
IGENERAL INFORMATION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
ITILE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
ITILE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
ITILING DATE: 1085 COMPATION: WORK TO THE GLGF
ITILING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PALENTION INTERACTION: 196
CURRENT APPLICATION NUMBER: US/08/681,219
FILING DATE: 22-UUL-196
CLASSIFICATION NUMBER: US/08/681,219
FRIEDENONE: (212) 278-0400
TELEPAN (212) 278-0400
TELEPANS (212) 319-0525
INFORMATION FOR SEQ ID NO: 15:
LENGTH; 13 amino acide
STRENDENSS: single
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US-10-015-39A-397
US-10-017-25AA-397
US-10-017-867A-397
US-10-012-101B-397
US-10-012-137A-397
US-10-012-754A-397
US-10-013-910A-397
US-10-013-910A-397
US-10-013-912A-397
US-10-015-65AA-397
US-10-015-67AA-397
US-10-015-67AA-397
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                                                                                                                                                                                                                                                                    APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, Junn
APPLICANT: Yanagisawa, Junn
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOWAIN AND USES THEREOF
FILE REFERENCE: 49862-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,111C
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
180 ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
PILE REFERENCE: 65823/JPW/PT
CURRENT PAPLICATION NUMBER: US/10/092,138
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09230111C Publication No. US20030203414A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/10092138
Publication No. US20030170723A1
GENERAL INFORMATION:
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                                                                                                                                                     FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:source:synthesized
                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:source:synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                         ENGTH: 13
                                                                          Local Similarity
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1 SDSNMNMNELSEV 13
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                                                      13; Conservative
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Pred. No. 9.7e-05;
                                                                        Score 64; DB 12;
Pred. No. 9.7e-05;
                                                        Mismatches
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                                                                          ; ORGANISM: Eucalyptus grandis US-10-101-464A-905
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US-10-101-464A-905
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PRIOR FILING DATE: 2000-11-01
PRIOR PPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
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LENGTH: 126
TYPE: PRT
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Publication No. US20030046728A1
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nico
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                Query Match
Best Local Similarity
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Best Local :
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TITLE OF INVENTION: Compositions Isolated from Plant Cells.
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
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APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
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CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
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                                                                                                                  TYPE: PRT
                                                                                                                                     LENGTH: 412
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les 8; Conserv
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72.7%;
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Pred. No.
                  Score 39;
Pred. No.
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              DB
85;
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US-10-101-464A-955
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                                                                                   SOPTWARE: Pa
SEQ ID NO 977
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Best Local Similarity
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ORGANISM: Eucalyptus grandis
-10-101-464A-977
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APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: FCT/US00/00724
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GENERAL INFORMATION:
                                                                                                                                                                                       APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
PILE REFERENCE: 11000.1020C2
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/728,986
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-11-01
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                                                                                                   NUMBER OF SEQ ID NOS: 989
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US00/00724 PRIOR FILING DATE: 2000-01-11
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                                         TYPE: PRT
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o. US20030046728A1
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72.7%;
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Pred. No. 1e+02;
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APPLICANT: HOLTZMAN, DOUGLAS A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
FILE REFERENCE: MPI00-5350MNIM
CURRENT APPLICATION NUMBER: US/09/759,130B.
CURRENT APPLICATION NUMBER: US/09/479,249
FRIOR APPLICATION NUMBER: US/09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US/9/559,497
PRIOR APPLICATION NUMBER: US/9/559,497
PRIOR APPLICATION NUMBER: US/9/559,497
PRIOR APPLICATION NUMBER: US/9/559,497
PRIOR APPLICATION NUMBER: US/9/578,063
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-05-24
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SEQ ID NO 7531
LENGTH: 639
TYPE: PRT
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
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Publication No.
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Best Local Similarity
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Terry, Roen APPLICANT: Bo, Jiang APPLICANT: Charles, I APPLICANT: Howard, Bu
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NUMBER OF SEQ ID NOS: 8000
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NAME/KEY: MISC FEATURE
LOCATION: (639)..(639)
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Similarity 63.6%;
7; Conservati
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                                                                                                                                                                                                                                                                                                                                                                                    McCarthy, seam ...
Fraser, Christopher C
                                                                                                                                                                                                                                                                                             Mackay, Charles R
Myers, Paul S
                                                                                                                                                                                                                                                                                                                                      Barnes, Thomas
Kirst, Susan J
                                                                                                                                                                                                                                        Wrighton, Nicolas
Goodearl, Andrew
                                                                                                                                                                                                                                                                                                                                                                          Fraser, Christ
Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l, Application US/10032585
vo. US20030180953A1
                                                                                                                                                                                                                                                                                 Leiby, Kevin R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09759130B
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                                                                                                                                                                                                                                                                                                                                                           Thomas S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 15;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 639;
4.5e+02;
ches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 997
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                                                                                                                                                                                        THERAPEUTIC,
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                                                                                                                                                                                          AND OTHER
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APPLICATION NUMBER: US 09/333,159

1999-06-14 2000-07-14

FILING DATE:

FILING DATE: 1999-06-29

APPLICATION NUMBER: US 09/342,364 APPLICATION NUMBER: US 09/596,194

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Best Local Similarity
"-*-hes 7; Conserv
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PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR APPLICATION NUMBER: US 09/33,159
PRIOR APPLICATION NUMBER: US 09/33,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 196
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HOLTZMAN, DOUGLAS A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
TITLE OF INVENTION: USES.
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                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Millennium Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: MPI00-5350MNIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                       APPLICATION NUMBER: US 09/608,452 FILING DATE: 2000-06-30
                                                                                                                               FILING DATE: 2000-07-14
APPLICATION NUMBER: US 09/342,364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/420,707
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FILING DATE: 2000-06-23
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APPLICATION NUMBER: US 09/602,871 FILING DATE: 2000-06-23
                                    FILING DATE:
                                                     APPLICATION NUMBER: US 09/393,996
                                                                                                              FILING DATE: 1999-06-29
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Goodearl, Andrew
Holtzman, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barnes, Thomas
Kirst, Susan J
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Fraser, Christopher C
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0. US20030022279A1
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                                  1999-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charles R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas S
                                                                                                                                                                                                                                                                                                                                                                                                                                PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.7%;
53.8%;
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Pred. No.
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Best Local S
Matches 7
                                                                                                                                                                                                                                  Sequence 193, Applic
Publication No. US20
GENERAL INFORMATION:
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SEQ ID NO 218
LENGIH: 348
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NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 195
LENGTH: 337
TYPE: PRT
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Publication No.
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Best Local
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                               APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                  APPLICANT: Millennium Pharmaceuticals, APPLICANT: McCarthy, Sean A
                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 08/902,615 PRIOR FILING DATE: 1997-07-29
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TITLE OF INVENTION:
                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter pylori
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les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 SDVNLSHNQLREV 130
                                                                                                                                                                                                                                                                                                                                                         63
T: Goodearl, Andrew
T: Holtzman, Douglas A
INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T: Ocomen, Raymond P.
INVENTION: Identification of Polynucleotides
INVENTION: Encoding No. US20030158396Aiel H
                                                                                                                                                                                                                                                                                                                                                                                         1 SDSNMNMNE 9
                                                                                                Barnes, Tnome
Kirst, Susan J
Kirst, Charles R
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                          McCarthy, Seam A
Fraser, Christopher C
                                                                                                                                                                 Fraser, Christ
Sharp, John D
                                                                  Leiby, Kevin R
Wrighton, Nicolas
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5. US20030022279A1
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o. US20030158396A1
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 12;
Pred. No. 3.4e+02;
2; Mismatches 1
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Pred. No. 3.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 348;
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   THERAPEUTIC, AND OTHER
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RESULT 13
US-09-946-374-397
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; ORGANISM: Homo sapiens
US-09-759-130B-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 397, Appublication No.
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LENGTH: 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830P1C1 CURRENT APPLICATION NUMBER: US/09/946,374 CURRENT FILING DATE: 2001-09-04 PRIOR APPLICATION NUMBER: 60/098716
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
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CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
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FILING DATE: 2000-05-24
APPLICATION NUMBER: US 09/333,159
FILING DATE: 1999-06-14
APPLICATION NUMBER: US 09/596,194
FILING DATE: 2000-07-14
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APPLICATION NUMBER: US 09/420,707
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FILING DATE: 1999-06-29
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                                                                                                                                                                                                                                                                        Roy, Ma
Smith,
                                                                                                                                                    Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                 Paoni,
                                                                                                                                                                                                                                                                                                                                          Pan, James
                                                                                                                                                                                                                                                                                                                                                             Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                           Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Botstein, David
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o. US20030073129A1
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                                                                                                                                                                                                                                                                 ni, Nicholas F., Margaret Ann
th, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dan L.
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                                                                                                                                                                                                                          Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 11;
Pred..No. 3.4e+02;
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PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION UNMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
                                                                                                   OR APPLICATION NUMBER: 60/100710
OR FILING DATE: 1998-09-17
OR APPLICATION NUMBER: 60/100711
OR FILING DATE: 1998-09-17
OR APPLICATION NUMBER: 60/100848
OR FILING DATE: 1998-09-18
OR APPLICATION NUMBER: 60/100849
OR APPLICATION NUMBER: 60/100919
OR APPLICATION NUMBER: 60/100919
OR APPLICATION NUMBER: 60/100919
OR FILING DATE: 1998-09-17
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OR APPLICATION NUMBER: 60/099741
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099754
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099763
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099792
OR APPLICATION NUMBER: 60/099792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR FILING DATE: 1998-09-10

PR APPLICATION NUMBER: 60/099812

PR FILING DATE: 1998-09-10

PR APPLICATION NUMBER: 60/099815

PR FILING DATE: 1998-09-10

PR FILING DATE: 1998-09-10

PR APPLICATION NUMBER: 60/100385

PR FILING DATE: 1998-09-15

PR APPLICATION NUMBER: 60/100388

PR FILING DATE: 1998-09-15

PR APPLICATION NUMBER: 60/100390

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PR APPLICATION NUMBER: 60/100390

PR APPLICATION NUMBER: 60/100390

PR APPLICATION NUMBER: 60/100584

PR APPLICATION NUMBER: 60/100584

PR APPLICATION NUMBER: 60/100584
                                                          APPLICATION NUMBER: 60/100930 FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100683
FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/100627
FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100661
FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099602
FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-09-02
APPLICATION NUMBER: 60/099536
FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-09-01
APPLICATION NUMBER: 60/098750
FILING DATE: 1998-09-01
              APPLICATION NUMBER: 60/101014
FILING DATE: 1998-09-18
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APPLICATION NUMBER: 60/099808
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FILING

1998-09-18

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APPLICATION NUMBER: 60/101474

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1998-09-1998-09-1

60/101279 60/101071

APPLICATION NUMBER: 60/101471

NUMBER: 60/101472

1998-09-23

1998-09-23

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RESULT 14
US-10-015-387A-397
; Sequence 397, App
; Publication No. U
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                                                                                                                                                              Prior Application removed -
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 397
LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                               US-10-015-387A-397
                                                                    Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/015,387A CURRENT FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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OR FILING DATE: 1998-10-20
OR APPLICATION NUMBER: 60/105002
OR FILING DATE: 1998-10-20
OR APPLICATION NUMBER: 60/105104
OR RILING DATE: 1998-10-21
OR APPLICATION NUMBER: 60/105169
OR FILING DATE: 1998-10-22
OR APPLICATION NUMBER: 60/105266
OR FILING DATE: 1998-10-22
OR APPLICATION NUMBER: 60/105693
OR APPLICATION NUMBER: 60/105693
OR APPLICATION NUMBER: 60/105694
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OR FILING DATE: 1998-10-08
OR APPLICATION NUMBER: 60/103711
OR FILING DATE: 1998-10-08
OR APPLICATION NUMBER: 60/104257
OR FILING DATE: 1998-10-14
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 134
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                                                                      Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
SDVNLSHNQLREV 146
                                    SDSNMNMNELSEV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                     Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                    Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ferrara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eaton, Dan 1
                                                                                                                                                                                                                                                                                                                                                                                      Pan, James
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5. US20030135034A1
                                                                        Conservative
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                                                                      Score 35; DB 12;
Pred. No. 3.4e+02;
3; Mismatches 3;
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Pred. No. 3.4e+02;
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                                                                                                           Length 353;
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APPLICATION NUMBER: 60/103633

APPLICATION NUMBER: 60/103449

FILING DATE:

1998-10-07

FILING DATE: 1998-10-07 APPLICATION NUMBER: 60/103401

APPLICATION NUMBER: 60/103396 FILING DATE: 1998-10-07

FILING DATE: 1998-10-07 APPLICATION NUMBER: 60/103395

APPLICATION NUMBER: 60/103328

1998-10-07

FILING DATE:

FILING DATE: 1998-10-07 APPLICATION NUMBER: 60/103315

APPLICATION NUMBER: 60/103314

1998-10-06 1998-10-02

60/103258

FILING DATE: 1998-10 APPLICATION NUMBER:

FILING DATE:

FILING DATE: 1998-10-01 APPLICATION NUMBER: 60/102965

APPLICATION NUMBER: 60/102687 FILING DATE: 1998-10-01

FILING DATE: 1998-09-30
APPLICATION NUMBER: 60/102684

APPLICATION NUMBER: 60/102571

APPLICATION NUMBER: 60/102570

1998-09-30

FILING DATE:

FILING DATE:

FILING DATE: APPLICATION NUMBER: FILING DATE:

APPLICATION NUMBER: 60/102331

60/102484

FILING DATE:

FILING DATE:

FILING DATE:

FILING DATE:

APPLICATION NUMBER: 60/102207

APPLICATION NUMBER: 60/101916

1998-09-24

APPLICATION NUMBER: FILING DATE:

FILING DATE: 1998-09-24

APPLICATION NUMBER: 60/101743

1998-09-24

60/101915

APPLICATION NUMBER: 60/101741 APPLICATION NUMBER: 60/101738

1998-09-24

FILING DATE: 1998-09-24

FILING DATE: APPLICATION NUMBER: FILING DATE:

1998-09-23

60/101479

FILING DATE: 1998-09-23 APPLICATION NUMBER: 60/101477 APPLICATION NUMBER: 60/101476

1998-09-23

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1998-09-23 1998-09-23

60/101475

FILING DATE:

APPLICATION NUMBER: 60/102240

1998-09-29 1998-09-29

APPLICATION NUMBER: 60/102330 FILING DATE: 1998-09-29 APPLICATION NUMBER: 60/102307

APPLICATION NUMBER: 60/102487

1998-09-30 1998-09-30 1998-09-29 1998-09-29

FILING DATE: APPLICATION |

1998-10-08

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RESULT 15
US-10-006-130A-397
| Sequence 397, Application US/10006130A
| PULICATION NO. US20030148375A1
| GENERAL INFORMATION |
| REPLICANT: Bear, Kevin P. |
| APPLICANT: Bear, Mapleone |
| APPLICANT: Goddard, Andrey |
| APPLICANT: Goddard, Machael |
| APPLICANT: Goddard, Machael |
| APPLICANT: Beand, Micholas P. |
| APPLICANT: Beand, Micholas P. |
| APPLICANT: Pan, James |
| APPLICANT: Colone |
| APPLICANT: Pan, James |
| APPLICANT: Colone |
| APPLICANT: Pan, James |
| APPLICANT: Pan, James |
| APPLICANT: Goddard, Andrey |
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Maximum DB
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Perfect score:
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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64
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

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// SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:
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// SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:
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// SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
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57.280 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

9	œ	7	o,	(J)	4	w	N	L	Result No.
39	39	39	39	39	39	39	42	64	Score
60.9	60.9	60.9	60.9	60.9	60.9	60.9	65.6	100.0	Query Match
509	453	412	323	274	236	126	1072	13	% Query Match Length DB ID
23	24	21	22	17	13	21	22	19	DB . ID
ABP65470	ABP79742	AAB25530	ABG24842	AAW14864	AAR24191	AAB25497	AAG70871	AAW50176	Ĭ
Bifidobacterium lo	N. gonorrhoeae ami	Eucalyptus grandis	<ul> <li>Novel human diagno</li> </ul>	Subtilisin DY vari	Bovine RSV strain	Eucalyptus grandis	C albicans apoptos	Signal-transducing	Description

4

Inhibition of signal transduction - by inhibiting binding between a signal-transducing protein and a cytoplasmic protein, for treating

		3 21	313		35	45
Arabidopsis thalia			31.	4	35	44
C. pneumoniae prot	) AAY35667		27:	4.	35	43
Arabidopsis thalia			25	4	35	42
Arabidopsis thalia	. AAG07837		25	4.	35	41
Helicobacter pylor			20.	4	3 5	40
Human protein sequ			15	4	35	39
Protein involved i			14	4.	35	38
Arabidopsis thalia			14:	4.	35	37
Human ORFX protein			12	Α.	35	36
Human ORFX ORF205			12	4	35	35
Human ORF69 protei			9	4	35	3 4
Human ORFX protein			9	4	35	33
Novel human diagno			198	9	36	32
Drosophila melanog			155	ġ	36	31
Arabidopsis thalia			104	ġ	36	30
Protein L. Peptoc			102	ò	36	29
Protein L. Peptoc			102	ō	36	28
Polyprotein (pol)	. AAB03129		995	56.2	36	27
Era			79!	'n	36	26
G6PD. Plasmodium			75:	Ģ	36	25
Plasmodium falcipa			71:	Ġ	36	24
Candida albicans e			63	9	36	23
Novel human diagno			62	9	36	22
P. falciparum spor			49	•	36	21
Plasmodium falcipa			45,	٥,	36	20
Novel human diagno			44	٥,	36	19
Helicobacter pylor			370	რ	36	18
Sequence of Plasmo			33;	ი	36	17
Drosophila melanog			109.	7.	37	16
Zea maya protein f	. AAG35196		42	.7	37	15
8ophi			40	7.	37	14
Zea mays protein f			38	7.	37	13
			31,	7.	37	12
Zea mays protein f			111	7.	37	11
Novel human diagno	ABG24846	5 22	100	60.9	39	10

## ALIGNMENTS

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RESULT 1
AAMSOIT
ID AAMSO
XX AAMS
XX AAMS
XX AAMS
XX Inhi
KW Inhi
KW cytco
KW vira
XX Vira
XX Synt
XX 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibition; specific binding; signal-transducing protein; cytoplasmic protein; proliferation; cancer cell; apoptosis; virally infected cell.
                                                                                                   Sato T, Yanagisawa J;
Sato<sup>#</sup>T/, Yanagisawa J;
WPI; 1998-145347/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal-transducing protein carboxy-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW50176;
                                                                                                                                                                                                                                                                                                                                                               22-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9805347-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW50176 standard; peptide;
                                                                                                                                                                                                                                                (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                               96US-0681219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US12677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
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RESULT 2
AAG70871
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                              The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between a signal-transducing protein (STP) having the carboxy-terminal sequence (Ser/Thr)-Xaa-(Val/Ile/Leu), where Xaa = any amino acid (e.g. the present peptide), and a cytoplasmic protein (CP) containing the sequence AAW50162 or AAW50163. The composition can be used to inhibit the proliferation of cancer or virally infected cells, or induce apoptosis in cancer or viralls infected cells.
Sequence
                                                                                                                                                    Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases -
                                                                                                                                                                                                                                                        Contreras RH,
Nelissen BJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast; fungus; apoptosis; infection; proliferative disease; vaccine; autoimmune disease; ischaemia; neurodegeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG70871 standard; Protein; 1072 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g.
                                                                                                                             Claim 24;
                                                                                                                                                                                                                    WPI; 2001-367042/38.
N-PSDB; AAH29907.
                                                                                                                                                                                                                                                                                                                                               03-JUL-2000; 2000WO-BE00077
                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                           Candida albicans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                 WO200102550-A2
                                                                                                                                                                                                                                                                                              (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                       neurodegeneration.
eins of the inventi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  composition is capable of inhibiting specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDSNMNMNELSEV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDSNMNMNELSEV 13
                                                                                                                           Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 AA;
1072 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                             2
                                                                                                                                                                                                                                                        De Backer MD,
Reekmans RJ;
                                                                                                                                                                                                                                                                                                                      99EP-0870141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral infection
                         invention
                                                                                                                           218pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells, or induce apoptosis in cancer or virally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated
                                   The present
                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64;
Pred. No.
                                                                                                                                                                                                                                                                   Luyten WHML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                     sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.00011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
                                                                                                                                                                                                                                                                     Malcorps IKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                   one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                     the C. albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Query Match

65.6%;

Score

42;

DB

22;

Length 1072;

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DSNMMMNELSE

12

DSNMTSNEASE

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cc and protein sequences isolated from eucalyptus (Eucalyptus granus, ... cc pine (Pinus radiata also known as Monterey pine). The protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and cc development of a plant. They can be used to modify cell proliferation, cc differentiation, elongation and survival, resistance to disease and cmutrient metabolism. Examples of modifications which can be produced are cc altered fruit ripening and senescence of leaves and flowers e.g. to cd day senescence and prolong the life of cut flowers or enhance cc modifications can be used to engineer sterile plants. Other cc organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in cc forest tree species giving long stretches of valuable knot free clear cc wood which can be used in solid timber furniture and veneers.
                                                             XYXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 53.8%;
Matches 7; Conservative
                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 389; 527pp;
                                                                                                                                                                                                                                                                                                                                                                                               CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eucalyptus grandis; Pinus radiata; Monterey p: plant cell signalling; modulation; transgenic environmental change; development; cell prolli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB25497 standard;
                                                                                                                                                                                                                                                                                                                   AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-476052/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2000; 2000WO-US00724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elongation; survival;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eucalyptus grandis cell signalling involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB25497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD.
Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            external signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDSNMNMNELSEV 13
                                                             126 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nieuwenhuizen NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0228986
99US-0162866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 126 AA
               60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease resistance; nutrient metabolism
                                                                                                                                                                                                                                                                                                                                                                  English.
 0;
               Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                 DB
34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferation;
                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pine; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant;
                             Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:816
   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
   0
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RESULT 5
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Best Local S
Matches 6
                                                       subtilisin DY;
                                                                         Subtilisin DY variant A186N/S187D/F188Q/S190E
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                  This is the sequence of bovine respiratory syncytial virus (BRSV) strain FS-1 phosphoprotein (P) protein. It can be used in the detection of BRSV antibodies and in vaccines to prevent infection It can also be used for the production of BRSV protein antibodies see also AAR24185-R24190 and AAR25310. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                         Bovine respiratory syncytial virus agents for use in detection and as
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ25034.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Samal SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1992.
19-SEP-1996
                  WO9628557-A2
                                                                                               16-MAY-1997
                                                                                                                                   AAW14864 standard; protein; 274
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-183675/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine respiratory syncytial virus; vaccine; diagnosis; antibodies; P gene; phosphoprotein; BRSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine RSV strain FS-1 P protein.
                                                                                                                                                                                                                                                                                                                                                        Claim 33; Page 59; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9207940-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
24-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR24191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR24191 standard, Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAMA/) SAMAL S
                                                                                                                                                                                    52
                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                    TSTNONINQLSEI 64
                                                                                                                                                                                                       SDSNMNMNELSEV 13
                                                                                                                                                                                                                                                                  236 AA;
                                                                                                                                                                                                                          Conservative
                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                       variant; protease; cleaning composition; detergent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0608937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91WO-US08177
                                                                                                                                                                                                                                                                                                                                                                                                                                                        *
                                                                                              entry)
                                                                                                                                                                                                                                    60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                    B
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                    . 39,
                                                                                                                                                                                                                                                                                                                                                                          genes - used in the prodn. of vaccines for BRSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain FS-1
                                                                                                                                                                                                                                   DB
72;
                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                             Length 236;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                       t infection antibodies
                                                                                                                                                                                                                         0
                                                                                                                                                                                                                         Gaps
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RESULT 6
ABG24842
ID ABG2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
New isolated polynucleotide and encoded polypeptides, diagnostics, forensics, gene mapping, identification c
                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New subtilisin DY variants are provided in which one or more amino acids within one or more of the six Loop Regions have been replaced amino acids which are neutral or negatively charged and which are equally or (preferably) more hydrophilic than the corresponding ami acids in the wild-type sequence (see AAW03552).

Compared with wild-type Subtilisin DY, the variants have decreased adsorption to, and provide increased hydrolysis of, insoluble prote soils. They are useful as a component in a variety of cleaning compositions. The present sequence is a specific example of a
                                      N-PSDB;
                                                                            Drmanac RT, Liu C,
                                                                                                                              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                              11-OCT-2001.
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                  Novel
                                                                                                                                                                                                                                                                                                                                            18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                              ABG24842 standard; Protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subtilisin DY variants having amino acid substitutions in loops - are useful in cleaning compsns. having decreased adsorption ar increased hydrolysis and giving improved cleaning performance.
                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-433829/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barnett BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variant enzyme suitable for use in a granular fabric cleaning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examples 39-40; Page 131; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAR-1996;
                                                                                                      (HYSE-) HYSEQ INC.
                                                   2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 DSNKNRNDQSEV 191
                                                                                                                                                                                                                                                                                                               human diagnostic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                        AAS89029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROCTER & GAMBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSNMMNELSEV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brode PF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0401575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US03006
                                                                          Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rubingh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                             Ţ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                  #24833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
 , useful in of mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 7
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CC Sepecification, but was obtained in electronic format directly from WIPO care the value of the content of the printed of the content of 
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Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified repeaternal signals -
                                                                                                                                                                                                                                                                                                                                                     12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eucalyptus grandis; Pinus radiata; plant cell signalling; modulation; environmental change; development;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                     (GENE-)
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; modulation; transgenic plant; pathogen; growth;
development; cell proliferation; differentiation;
disease resistance; nutrient matholic.
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The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins are antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pline (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumer or to decrease hearth from the pathology of the life of the pathology 
                                                                                                                                                                                                                                                                                                          Disclosure; Page 626; 815pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria gonorrhoeae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N. gonorrhoeae amino acid sequence SEQ ID 6014.
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                             CC Bequence of a Bifidobacterium genome selected from the nucleotide CC sequences given in ABQB1842 and ABQB1843, or a sequence exhibiting at CC least 90% identity or which hybridises with the sequence given in CC ABQB1842 and ABQB1843. Also described is a polynucleotide (II) encoding CC ABQB1842 and ABQB1843. Also described is a polynucleotide (II) encoding CC given in ABP6528 to ABP66354 ligated in frame to a polynucleotide CC encoding a heterologous polypeptide. (I) has antidarrheic and CC (I) (which is a probe) is useful for the detection and/or identification of Bifidobacterium longum in a biological sample. A carrier containing CC the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) CC can be used for preventing and/or treating diarrhoea brought about by CC pathogenic bacteria and/or rotavirus. The carrier is a food composition CC delected from milk, yogurt, curd, cheese, fermented milk, milk based CC based powders, infant formula, pet food or a pharmaceutical composition CC supplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the carrier the affidobacterium related nucleotide sequences given in the Sequence CC Listing from the present invention but not mentioned further within the connection but not mentioned further within the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a polynucleotide (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID 214; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample, -
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                                                  CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC constitutes are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC conditions of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 55205; 103pp; English
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AAG35198

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XX Prote KW hybbi

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RESULT 13 AAG35197

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99US-0139459. 99US-0139460.	99US-0139457. 99US-013945B					55	3.53		<i>E</i> .	5.5	908-01	9US-01		908-01		908-01	9US-01	9US-01	9US-01:	908-01	9US-01	9US-01	9US-01	905-01:	9US-01	9US-01:	9US-01	9US-01	9US-01:	9US-01:		9US-01:	9US-01:	9US-01:	9US-01:	99US-0126264.	905-0125	99US-012318U. 99US-0123548.	9US-01218	2000EP-0301439.				o. mays.		netic mapping; gene expression control; orn.	signal transdu	ein fragment SEQ ID NO: 42962.	(first encry)			lard, Protein, 380 AA.
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272 SDEMVSMNEMAEI 284
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           (first entry)
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46.2%;
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Pred. No. 2.8e+02;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic a genes from Drosophila interactions -
06-SEP-2000.
                                                                                    Zea mays subsp.
                                                                                                                                termination sequence;
                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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N-PSDB; ABL04477.
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11-JUL-2000; 2000US-0614150.
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## ALIGNMENTS

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RESULT 1
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                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93211298; PunMed-8096320; Sohel I., Puente J.L., Murray W.J., Vuopio-Varkila J., Schoolnik G.K. "Cloning and characterization of the bundle-forming pilin gene of enteropathogenic Escherichia coli and its distribution in Salmonella serotypes.";
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major structural subunit of bundle-forming pilus
forming pilin) (Bundlin).
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MEDLINE=92054556; PubMed=1683004;
Giron J.A., Ho A.S.Y., Schoolnik G.K.;
"An inducible bundle-forming pilus of enteropathogenic Escherichia
                                                                                                                     EMBL; U27184; AAC44040.1;
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STRAIN=O111:H- / B171;
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Enterobacteriaceae; Escherichia.
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                                                                                   InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF05307; Bundlin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 254:710-713(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=168927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pB171.
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                                                                                                                                                                                                                                                                                                   FUNCTION: Major repeating bundle-forming pilus (BFP) subunit. Is required for EPEC localized adherence. SUBUNIT: 10 to 100 laterally aligned filaments or bundle-forming pili coalesce into rope-like bundles. These form linkages between the bacteria within the enteropathogenic E.coli (EPEC) microcolonies that are attached to epithelial cells. SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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                                                                                                                                                                                                                                                      a collaboration
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PROSITE; Fimbria;

PS00409; PROKAR NTER METHYL; Methylation; Plasmid.

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MAJOR STRUCTURAL FORMING PILUS

SUBUNIT OF BUNDLE-

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CONFLICT
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Pfam; PP05307; Bundlin; 1.
PROSITE; PS00409; PROKAR NTER METHYL; 1.
Fimbria; Methylation; Plasmid; 3D-struct
                                                                                                                                                                                                                                                                                              PIR; S70966; S70966.
PDB; 1QT2; 12-JUL-99.
                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=0127:H6 / E2348/69;
MEDLINE=93133122; PubMed=1362446;
Donnenberg M.S., Giron J.A., Nataro J.P., Kaper J.B.;
Pa plasmid-encoded type IV fimbrial gene of enteropathogenic
"A plasmid-encoded type IV fimbrial gene of enteropathogenic
Escherichia coli associated with localized adherence.";
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SUBUNIT: 10 to 100 laterally aligned filaments or bundle-forming pili coalesce into rope-like bundles. These form linkages between the bacteria within the enteropathogenic E.coli (EPEC) microcolonies that are attached to epithelial cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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sen the Swiss Institute of Bioinformatics and the EN
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7-46 / E2348/69;
7-5-Med=10
Similarity
8; Conserv
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(Rel. 42, Last annotation update)
tural subunit of bundle-forming pilus
  Conservative
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                   Score 40;
Pred. No.
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Pred. No.
                                                                                                         POTENTIAL
                                                                                                                        MAJOR STRUCTURAL SUBUNIT OF BUNDLE-
FORMING PILUS.
METHYLATION (POTENTIAL).
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POTENTIAL.
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                                                                                                                                                                                  RA Kunst F. Ogsawara N. Moszer I. Albertini A.M., Alloni G.,
RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A.M., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA McDia B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Minuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S. H.,
RA Parescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Riger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan S., Vandenbol H., Vannier F., Vasaarotti A.,
RA Vasakoka A., Tanaka T., Terpstra P., Tognoni A.,
RA Tokeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Vasarotti A.,
RA Vashida K., Yoshikawa H.F., Zumstein B., Woshikawa H., Danchin A.,
RA Winter S., Winter S., Wedler H., Wather S., Vata K.,
Nahata Ra Winter S., Wata A., Vasanoto M., Vata K.,
Nahata Ra Winter S., Wat
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P07343; O321
01-APR-1988
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SEQUENCE OF
STRAIN=168;
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                                                                                                       Nature 390:249-256(1997).
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Bacteria; Firmicutes;
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30-1APR-1988 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fumarate hydratase, class-II (EC 4.2.1.2) (Fumarase)
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HSSP; P05042; 1FUR.
Subtilist; BG10384; citG.
InterPro; 1PR005677; Fum_hydII.
InterPro; 1PR000362; Fumarate_lyase.
Pfam; PF00206; lyase_1; 1.
PRINTS; PR00149; FUMRATELYASE.
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FUMC_CAMJE
069294;
16-0CT-2001
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ACT_SITE
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EMBL; AJ223978; CAAL1749.1; -.
EMBL; Z99120; CAB15294.1; -.
EMBL; M11918; AAAZ2464.1; -.
EMBL; Z93941; CAB07973.1; -.
Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                           FUMC OR CJ1364C
                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fumarate hydratase class II (EC 4.2.1.2) (Fum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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Price V.A., Feavers I.M., Moir A.;
Proce of sigma H in expression of the fumara
vegetative cells of Bacillus subtilis 168.";
J. Bacteriol. 171:5933-5939(1989).
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Peavers I.M., Miles J.S., Moir A.
"The nucleotide sequence of a spo-
Bacillus subtilis 168.";
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Tricarboxylic acid Gycle; Complete proteome.

TE 186 POTENTIAL.

G 322 SUBSTRATE CARBOXYL (PC G 322 322 SUBSTRATE CARBOXYL (PC G 66 66 A -> V (IN REF. 1).
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Pred. No. 15;
2; Mismatches
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A -> V (IN REF. 1).
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and citG (289
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STRAIN=NCTC 11168;
Griffiths P.L., Conne
Submitted (MAR-1998)
                                                                                                                                           Escherichia coli.
Bacteria, Proteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jeju
reveals hypervariable sequences.";
Nature 403:665-668(2000)
                       SEQUENCE FROM N.A. STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRAMS; TIGRO0979; fumC II; 1.

PROSITE; PS00163; FUMARATE LYASES; 1.

LYASE; Tricarboxylic acid Cycle; Complete proteome.

ACT_SITE 187 187 POTENTIAL.

BINDING 323 323 SUBSTRATE CARBOXYL (PC SEQUENCE 463 AA; 50710 MW; E281B37B5791FFC0 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
MEDLINE=87099873; PubMed=3541901;
                                                                                            NCBI_TaxID=562;
                                                                                                                         Enterobacteriaceae;
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InterPro; IPR000362; Fumarate_lyase.
Pfam; PF00206; lyase_1; 1.
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-!- PATHWAY: Tricarboxylic acid cycle.
-!- SUBUNIT: Homotetramer (By similarity)
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HSSP; P05042; 1FUR.
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he EMBL/GenBank/DDBJ databases
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SUBSTRATE CARBOXYL (POTENTIAL)
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Nucleic Acids Res. 12:3631-3642(1984)
[5]
SEQUENCE OF 1-20.
MEDLINE-92011457; PubMed=1917897;
Ueda Y., Yumoto N., Tokushige M., Ful
"Purification and characterization of
Bscherichia coli.";
        Weaver T., Lees M., Banaszak L.;
"Mutations of fumarase that distinguish between the acmearby dicarboxylic acid binding site.";
Protein Sci. 6:834-842(1997).
-i- CATALYTIC ACTIVITY: (S)-malate = fumarate + H(2)O.
-i- PATHWAY: Tricarboxylic acid cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T. Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tayami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Meda C., Yamamoto Y., Horiuchi T., Escherichia coli K-12 genome 7A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.", DNA Res. 3:363-377(1996).
                                                                                                                         Biochemistry
                                                                                                                                                                                                          MEDLINE=88193096; PubMed=3282546; Woods S.A., Shwartzbach S.D., Guest J.R.; Woods S.A., Shwartzbach S.D., Guest J.R.; "Two biochemically distinct classes of fumarase in Biochim. Biophys. Acta 954:14-26(1988).
                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-15, AND CHARACTEKIZA
MEDLINE=93267645; PubMed=8496960;
Weaver T.M., Levitt D.G., Banaszak
"Purification and crystallization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of the Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=84221385; PubMed=6328431; Miles J.S., Guest J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
Mau B., Shao Y.;
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SEQUENCE FROM N.A
STRAIN=K12 / MG16
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                                                                                  MEDLINE=97253450; PubMed=9098893;
                                                                                               X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
                                                                                                                                                                       MEDLINE=97065812; PubMed=8909293;
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                                                                                                                       "Crystallographic studies of the catalytic fumarase C from Escherichia coli."; Biochemistry 35:13955-13965(1996).
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Science 277:1453-1474(1997).
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 SUBUNIT:
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EMBL; AB000256; AAC74633.1; -.
EMBL; D90803; BAA15349.1; -.
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EMBL; D90805; BAA15363.1; -.
EMBL; D90805; BAA15363.1; -.
EMBL; X00522; CAA25205.1; -.
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PDB; 1FUR; 23-JUL-97.
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EcoGene; EG10358; fumC.
InterPro; IPR005677; Fum_hydII.
InterPro; IPR00362; Fumarate_lyase.
Pfam; PF00206; lyase 1; 1.
PRINTS; PR00149; FUMRATELYASE.
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PRO0149; FUMRALEL...
Ms; TIGR00979; fumC II; 1.
ZE; PS00163; FUMARATE LYASES; 1.
ZE; PS00163; FUMARATE LYASES; 1.
Tricarboxylic acid cycle; 3D-structure; Comp...
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POTENTIAL.
SUBSTRATE CARBOXYL (POTENTIAL).
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RA Bargues M., Baron L., Becker A., Biteau N., Bloecker H., Blugeon C.,

RA Boskovic J., Barandt P., Brueckner M., Buitrago M.J., Coster F.,

RA Boskovic J., Barandt P., Brueckner M., Buitrago M.J., Coster F.,

RA Goffeau A., Gemez-Peris A., Granotier C., Hanemann V., Hankeln T.,

RA Hoheisel J.D., Jaeger W., Jimenez A., Jonniaux J.-L., Kraemer C.,

RA Hoheisel J.D., Jaeger W., Jimenez A., Jonniaux J.-L., Kraemer C.,

RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,

RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,

RA Pydz H., Purnelle B., Rasmussen S.W., Remacha M., Revuelta J.L.,

RA Prydz H., Purnelle B., Rasmussen S.W., Remacha M., Revuelta J.L.,

RA Rieger M., Salom D., Saluz H.P., Saiz J.S., Saren A.-M., Schaefer M.,

RA Rieger M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,

RA Wagner G., Wambutt R., Wedler E., Wedler H., Woelfl S., Harris D.E.,

RA Wagner G., Wambutt R., Wedler E., Wedler H., Woelfl S., Harris D.E.,

RA Wagner G., Wambutt R., Wedler E., Wedler H., Woelfl S., Harris D.E.,

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RA Wagner G., Wambutt R., Wedler E., Wedler H., Woelfl S., Harris D.E.,

RA Odell C., Oliver K., Rajandream M.A., Richards C., Shore L.,

RA Odell C., Oliver K., Rajandream M.A., Richards C., Shore L.,

RA Vales B., Berno A., Carpenter J., Chen E., Cherry J.M.,

RA Chang D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A.,

RA Caffer P., Oh C., Derel F X., Roberts D., Schwara S., Cherry J.M.,

RA Caffer P., Oh C., Derel F X., Roberts D., Schwara S., Schroeder M.
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GNP1 OR YDR508C OR D9719.14.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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NCBI_TaxID=4932;
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Davis R.W., Johnston M., Andrews S., Brinkman R., Cooper J., Ding H.,
Du Z., Favello A., Fulton L., Gattung S., Greco T., Hallsworth K.,
Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Kirsten J.,
Kucaba T., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
Miller N., Whan M., Pauley A., Peluso D., Rifkin L., Riles L.,
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
Wilson R., Waterston R., Albermann K., Hani J., Heumann K., Kleine K.,
Mewes H.-W., Zollner A., Zaccaria P.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IV.";
Nature 387:75-78(1997).
                                                     TRANSMEM
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                              InterPro; IPROU4/02,
Pfam; PF00324; aa permeases;
TIGRFAMS; TIGRO0913; 2A0310;
PROSITE; PS00218; AMINO ACID
PROSITE; PS00218; AMINO ACID
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SGD; S0002916; GNP1.
GO; GO:0015359; F:amino acid permease activity;
GO; GO:0006865; P:amino acid transport; IDA.
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InterPro; IPR004840; AAc_permease.
InterPro; IPR004841; Permease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10654085;
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    !- SIMILARITY: Belongs to the amino acid permease family.

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Leu, Ser, Thr, Cys, Met and Asn.
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RESULT 7
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01-AUG-1992 15-SEP-2003

(Rel. 23, Created)
(Rel. 23, Last sequence update)
(Rel. 42, Last annotation update)

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Johnston M., Hiller L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Entian K.-D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Wueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Vlaerendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; "The mucleotide sequence of Saccharomyces cerevisiae chromosome XII.", Nature 387:87-90(1997).
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PEP3 OR VPS18 OR YEX148W OR L9634.2.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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MEDLINE=92049306; PubMed=1840635;

MEDLINE=92049306; PubMed=1840635;

Robinson J.S., Graham T.R., Emr S.D.;

Robinson J.S., Graham T.R., Emr S.D.;

"A putative zinc finger protein, Saccharomyces cerevisiae Vps18p,

"A putative zinc finger protein, Saccharomyces cerevisiae Vps18p,

"A putative zinc finger protein, Saccharomyces cerevisiae Vps18p,

affects late Golgi functions required for vacuolar protein sorting
and efficient alpha-factor probormone maturation.";

Mol. Cell. Biol. 11:5813-5824(1991).
                                                                                                                                              EMBL; M65144; AAA34852.1; -.
EMBL; Z73320; CAA97720.1; -.
EMBL; U53879; AAB82382.1; -.
                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        use
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MEDLINE=97313267; PubMed=9169871;
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STRAIN=S288c / /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preston R., Manoison M.F., Becherer K., W. Kirkpatrick D., Wright R., Jones E.W.; "Isolation and characterization of PEP3, obiogenesis in Saccharomyces cerevisiae."; Mol. Cell. Biol. 11:5801-5812(1991).
                                                                                                                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                  This
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    ; A41943; A41943.
; S0004138; PEP3.
GO:0000306; C:extrinsic to vacuolar membrane; I GO:0000306; C:exturinsic to vacuolar membrane; I GO:0000329; C:vacuolar membrane (sensu Fungi); GO:0005515; F:protein binding activity; IMP. GO:0006895; P:Golgi to endosome transport; IGI. GO:0042145; P:homotypic vacuole fusion (non-aut
                                                                                                                                                                                                                                             Buropean Bioinformatics Institute. The by non-profit institutions as long iffied and this statement is not removed. It is requires a license agreement (See littles requires a license agreement)
                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: REQUIRED FOR VACUOLAR BIOGENESIS.
SUBCELLULAR LOCATION: CYTOSOLIC FACE OF THE VACUOLAR
SIMILARITY: Contains 1 clathrin repeat.
SIMILARITY: Contains 1 C3HC2-type zinc finger.
                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a casen the Swiss Institute of Bioinformatics and the EMBL
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          (non-autophagic); IDA
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RELX HORSE
P22969; Q28907;
01-AUG-1991 (Rel. 19, Created)
I 01-NOV-1997 (Rel. 35, Last seque
II 16-OCT-2001 (Rel. 40, Last anno
Prorelaxin precursor (RXN).
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Best Local S
Matches
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                                                                                                                                        Endocrinology 129:375-383(1991).

-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMAL
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED DISULFIDE BONDS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                    MEDLINE=91275796; PubMed=2055195;
Stewart D.R., Mevins B., Hadas E., Vandlen R.;
"Affinity purification and sequence determination of equine relaxin.";
                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There is use by non-profit institutions as long as it modified and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            MEDLINB=9535930; PubMed=7543295;
Klonisch T., Ryan P.L., Yamashiro S., Porter D.G.;
"Partial complementary deoxyribonucleic acid cloning of
messenger ribonucleic acid, and its localization within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Placenta;
EMBL; AB000201;
EMBL; S78800; A
                                                                                                                   This
                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 32-174 FROM N.A.
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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ZN_FING 826 851
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                                                                                                                                                                                                                                                                                                                                 placenta."
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                                                                                                                   SWISS-PROT entry is copyright. It is produced through
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.918 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      iota K., Ogawa T.;
cloning of equine preprorelaxin
Dev. 42:171-178(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
 AAB35036.1;
                                                                                                                                                                                                                                                                                                                     52:1307-1315(1995)
            BAA19069.1;
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77.8%;
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Pred. No.
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V; 37AE3C34AE0470B8 CRC64;
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Best Local S
Matches 6
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PIR; C90176; C90176.
HAMAP; MF_00021; -; 1.
InterPro; IPR003720; Thil.
InterPro; IPR004114; THUMP_dom.
Pfam; PF02568; Thil; 1.
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28-FEB-2003
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAINATICG 35092 / DSM 1617 / P2;

MEDLINE=2132296; PubMed=11427726;

MEDLINE=21332296; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

-I- FUNCTION: Required for the synthesis of the thiazole moiety (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable thiamine biosynthesis protein thil.
THII OR SS00333.
                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobus solfataricus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                similarity).

PATHWAY: Thiamine biosynthesis.

SUBCELUTIAR LOCATION: Cytoplasmic (Potential).

SIMILARITY: BELONGS TO THE THII FAMILY.
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CONNECTING PEPTIDE.
RELAXIN A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB Pred. No. 18; 2; Mismatches
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L -> Q (IN REF. 2).
, E5C9414303A838B8 CRC64;
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RESULT 10
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RESULT 11
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Thiamine b
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE-99120557; PubMed=9923682;
MEDILINE-99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D.,
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Carmel G.
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.
Tummino P.J., Caruso A., Urla-Nickelsen M., Mills D.M., Iv
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
                                                                                                                                                                                                                                                                       TIGRAMM; TIGRO0839; aspA; 1.
PROSITE; PS00163; FUMARATE_LYASES; 1.
Lyase; Complete proteome.
SEQUENCE 468 AA; 51937 MW; B7C620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a centre of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
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Nature 397:176-180(1999)
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09ZLI5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aspartate ammonia-lyase (EC 4.3.1.1) (Aspartase).
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HSSP; P04422; 1JSW.
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-!- SUBUNIT: Homotetramer (By similarity).
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Bacteria; Proteobacteria; Epsilonproteobacteria; Ca
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004708; ApsA.
InterPro; IPR000362; Fumarate_lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001491; AAD06167.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic sequence comparison of two unrelated gastric pathogen Helicobacter pylori.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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371 AA; 41
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41847 MW; (
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Pred. No. 52;
3; Mismatches
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Pred. No. 40;
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6D9F628AEEB63F44 CRC64;
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GN SECG O
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Matches
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence u
15-DEC-1998 (Rel. 41, Last annotation
Probable protein-export membrane prot
SECG OR BB0054.
Bacteria; Spirochaetes; Spirochaetale
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01-NOV-1997
16-OCT-2001
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STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Tomb J.-F., White O., Kerlavage A.R., Gill S., Dougherty B.A.

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., FitzGerald L.M., Fujii C., Bowman C., Watthey L., Wallin

Cotton N.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,

Venter J.C.,
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pylori.";
Nature 388:539-547(1997).
-i- CATALYTIC ACTIVITY: L-aspartate = fumanous control of the control of th
  SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
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ASPA OR HP0649.
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                   NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004708; ApsA.
InterPro; IPR000362; Fumarate_lyase.
Pfam; PF00206; lyase_1; 1.
PRINTS; PR00149; FUMRATELYASE.
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CE 468 AA; 51981 MW; 60111E869302836A CRC64;
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PS00163; FUMARATE_LYASES;
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97 (Rel. 35, Last sequence update)
91 (Rel. 40, Last annotation update)
ammonia-lyase (EC 4.3.1.1) (Aspartase).
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation updat
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P04544;
13-AUG-1987
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Protein transport; Translocation; Transmembrane; Complete TRANSMEM 1 31 POTENTIAL.

TRANSMEM 59 79 POTENTIAL.

SEQUENCE 125 AA; 14015 MW; E0C2775AC19CE8F7 CRC64;
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                         Collins P.L., Wertz G.W.;
"Nucleotide sequences of the 1B and human respiratory syncytial virus.";
Virology 143:442-451(1985).
                                                                                                                                                                                                                                                                                                                                                                            Human respiratory syncytial virus (strain A2).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11259;
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-!- SUBCELLULAR LOCATION: Integral membrane protein (By si-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               burgdorter:..,
Nature 390:580-586(1997).
Nature 390:580-586(1997).
                            "mRNA sequence of three respiratory syncytial virus two nonstructural proteins and a 22K structural prot
                                                                                    Elango N.,
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=86045905; PubMed=2998021;
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                                                                                                                                            SEQUENCE
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        nonstructural proteins
Virol. 55:101-110(1985).
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                                                                                    Satake M., Venkatesan
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(Rel. 05, Last sequence update)
(Rel. 36, Last annotation update)
al protein 1 (Nonstructural protein
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                                                                                                             PubMed=4009789
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                                                                                                                                                                                                                                                                                                                                                      VNS1 HRSVL
Q86306;
                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comparing the statement is not removed.
                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Nonstructural protein 1 (Nonstructural protein 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE FROM N.A.
MEDLINE=95266253; PubMed=7747420;
Connors M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R.,
"A cold-passaged, attenuated strain of human reppiratory
virus contains mutations in the P and L genes.";
           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                         Mazumder B., Dupuy L.C., McLean T., Barik S.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                       Human respiratory syncytial virus (subgroup A / strain Long). Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD009407; Pneumo_NS1; 1.
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Pfam; PF03438; Pneumo_NS1; 1.
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passaged human respiratory syncytial virus vaccine candidate results
from the acquisition of a single mutation in the polymerase (L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97187925; PubMed=9035372;
Crowe J.E. Jr., Firestone C.Y., Whitehead
Murphy B.R.;
                                                                                                                                                                                                      NCBI_TaxID=11260;
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Pred. No.
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Nonstructural protein.
SEQUENCE 139 AA; 15539 MW; EF
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                                                                                                                                                              modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Female specific 800 protein (FS800).
Schistosoma mansoni (Blood fluke).
Eukaryota, Metazoa: Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                               DOMAIN
                                                                                                                                         EMBL; J03999; AAA29883.1;
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a detween the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                              Schistosoma mansoni.";
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89181810; PubMed=2927441;
Reis M.G., Kuhns J., Blanton R., Davis A.H.;
"Localization and pattern of expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Puerto Rican;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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Pfam; PF03438; Pneumo_NS1; ]
                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                          . Biochem. Parasitol. 32:113-119(1989).
FUNCTION: FS800 is likely to have some function in the programmer or maintenance of the schistosome egg.

EVELOPMENTAL STAGE: Highest level only in mature worms,
                                                                                                                                                                                                                                                                     overlapping reading frames.
                                                                                                                                                                                                                                                                                   during egg production. MISCELLANEOUS: The two
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## ALIGNMENTS

C;Accession: T33318 R;Geisel, C.; Bradshaw, H.

submitted to the EMBL Data Library, May 1998 A;Description: The sequence of C. elegans cosmid

ZK1055

A;Description: The sequence of A;Reference number: Z21321

hypothetical protein ZK1055.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <HEI>
A;Eross-references: GB:AE004301; GB:AE003852; NID:g9656865; PIDN:AAF95447.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16981; biotype Bl Tor
C;Genetics:
                                                                                                                                                                               R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen A;Reference number: A02035; MUID:20406833; PMID:10952301
A;Accession: H82091
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
H82091
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A;Molecule type: DNA
A;Residues: 1-1475 <GEI>A;Residues: 1-1475 <GEI>A;CTOSS-references: EMBL:AF068721; PIDN:AAC19259.1; GSPDB:GN00023; CESP:ZK1055.1
A;Experimental source: strain Bristol N2; clone ZK1055
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A;Introns: 17/3; 218/2; 385/3; 486/3; 1124/3; 1212/3; 1400/2
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                     A; Gene: VC2303
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position:
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Pred. No.
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                                                                                                                                                                                                                                                                                                     Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellere,
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ere, P
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$70966
fimbrial protein class IV precursor - Escherichia correction class IV precursor - Escherichia correction class IV precursor; pilin class IV precursor; pilin class IV precises: Escherichia coli
C;Species: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
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A;Cross-references: GB:BA000007; PIDN:BAB36935.1; PID:g13362983; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                        RESULT 5
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of enterohemorrhagic Escherichia coli
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85912
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A99629;
A;Accession: H91067
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A; Residues: 1-347 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable site specific recombinase [imported] - Escherichia coli (strain 0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Z3945 [imported] -
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Best Local S
Matches 7
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Best Local S
Matches S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Escherichia coli
Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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Best Local (
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N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
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75.0%;
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No.
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11;
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13;
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                                                                                  precursor; pilin class IV precursor
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Potamousis,
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                                                                                                                      A;Cross-references: GB:AE000814; GB:AE000666; A;Experimental source: strain Delta H
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A; Residues: 1-317 < MTH>
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GIG

nucleic

acid sequence not

shown;

translation not shown

NID: g2621334; PIDN: AAB84789.1;

PID:g262133

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A;ACCESBACH.
A;MOLECULE type: DNA
A;Residues: 1-193 <DON>
A;Residues: 1-193 <DON>
A;Residues: 1-193 <DON>
A;Cross-references: EMBL:Z12295; NID:g41061; PIDN:CAA78167.1;
A;Cross-references: EMBL:Z12295; NID:g41061; PIDN:CAA78167.1;
A;Experimental source: plasmid pMAR2
A;Experimental source: plasmid pmaray, W.J.; Vuopio-Varkila, J.; (
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A;Molecule type: DNA
A;Residues: 1-149,'S',151-193 <SOH>
A;Residues: 1-149,'S',151-193 <SOH>
A;Residues: 1-149,'S',151-193 <MBL:L07028; NID:g1314250; PIDN:AAC44040.1; PID:g1314251
A;Cross-references: GB:U27184; EMBL:L07028; NID:g1314250; PIDN:AAC44040.1; PID:g1314251
A;Gienc, J.A.; Ho, A.S.Y.; Schoolnik, G.K.
Science 254, 710-713, 1991
A;Title: An inducible bundle-forming pilus of enteropathogenic Escherichia coli.
A;Reference number: A60871; MUID:92054556; PMID:1683004
A;Accession: A60871
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A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463 A;Accession: H69135
                                                                                                                     R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicalre, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                              C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                       protein kinase - Methanobacterium thermoautotrophicum (strain Delta C_\ellSpecies: Methanobacterium thermoautotrophicum
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A; Residues: 'M', 15-40, 'I' <GIR>
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A; Title: Cloning and characterization of the bundle-forming pilin gene of enteropathogen A; Reference number: S31203; MUID:93211298; PMID:8096320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 20, 325-337, 1996
A;Title: A cluster of fourteen genes from enteropathogenic A;Reference number: S70966; MUID:96310370; PMID:8733231
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Best Local S
Matches 8
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Genome: plasmid;
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Residues: 1-193 <STO>
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8; Conserv
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ol. 20, 325-337, 1996
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Carlson, L.K.; Donnenberg,
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Pred. No. 8.9;
2; Mismatches
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A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-50, N' cPRI>
R;Kunst, F:; Ogasawara, N.; Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, V.; Berter
C:; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamametoi, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Accession: A69600
D. Stranslore and School an
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C;Species: B
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A;Experimental source: strain 168
C;Comment: This is a class II fumarase; it is thermostable.
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Nucleic Acids Res. 13, 131-140, 1985
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A; Residues: 1-65,'A',67-462 < KUN>
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Bacteriol: 171, 5933-5939, 1989

Title: Role of sigma H in expression of the fumarase; Reference number: A33488; MUID:90036677; PMID:2509423; Recession: A33488
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Best Local S
Matches 7
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A;Gene: fumC; NMA1670
C;Superfamily: fumara:
C;Keywords: carbon-ox:
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C; Superfamily:
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A;Title: Complete genome sequence of the alkaliphilic ba
A;Reference number: A83650; MUID:20512582; PMID:11058132
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A; Residues: 1-462 < PAR>
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A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete DNA sequence of a serogroup A strain of Neisseria A;Reference number: A81775; MUID:20222556; PMID:10761919
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A;Molecule type: DNA
A;Residues: 1-467 <MOO>
A;Cross-references: EMBL:X04065; NID:g41512; PIDN:CAA27698.1; PID:g41513
A;Cross-references: EMBL:X04065; NID:g41512; PIDN:CAA27698.1; PID:g41513
A;Cda, Y.; Yumoto, N.; Tokushige, M.; Fukui, K.; Ohya-Nishiguchi, H.
J. Biochem. 109, 728-733, 1991
A;Title: Purification and characterization of two types of fumarase from Escherichia A;Reference number: PX0048; MUID:92011457; PMID:1917897
A;Accession: PX0048; MUID:92011457; PMID:1917897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-463 <PAR>
A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73791.1;
A;Experimental source: serotype O2, strain NCTC 11168
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A;Molecule type: DNA
A;Residues: 1-462 <TET>
A;Cross-references: GB:AE002495; GB:AE002098; NID:g7226690;
A;Cross-references: serogroup B, strain MC58
                                                                                                                                                                                              C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 01-Mar-2002 C;Accession: S07138; PS0181; S33825; E64917; A05151 R;Woods, S.A.; Miles, J.S.; Roberts, R.E.; Guest, J.R. Biochem. J. 237, 547-557, 1986 A;Title: Structural and functional relationships between fumarase and asparl A;Reference number: S07138; MUID:87099873; PMID:3541901 A;Accession: S07138
                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: fumarase C_i fumarate hydratase class II; C_iSpecies: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fumarate hydratase (EC 4.2.1.2) Cj1364c [imported] - Campylobacter jejuni ()
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: A81281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: C81082
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A;Accession: A81281
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E90918
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A; Molecule type: protein
A; Residues: 1-20 < UED.
A; Residues: 1-20 < UED.
R; Guest, J.R.; Miles, J.S.; Roberte, R.E.; Woods, S.A.
J. Gen. Microbiol. 131, 2971-2984, 1985
A; Title: The fumarase genes of Escherichia coli: location
A; Reference number: A92783; MUID:86142617; PMID:3005475
A; Contents: annotation; identification of structural gene
R; Weaver, T.M.; Levitt, D.G.; Banaszak, L.J.
R; Weaver, T.M.; Levitt, D.G.; Banaszak, L.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fumarase C [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: E90918
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A;Pathway: tricarboxylic acid cycle
A;Note: in E. coli three different fumarate hydratase genes (fumA, fumB, and fu A;Note: fumC-encoded fumarate hydratase is a thermostable and iron-independent C;Superfamily: fumarate hydratase
C;Superfamily: fumarate hydratase
C;Keywords: carbon-oxygen lyaee; heat-stable protein; homotetramer; hydro-lyase F;278/Active site: His #status predicted
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A;Gene: fumC
A;Map position: 35.5 min
A;Map position: 35.5 min
A;Note: the gene coding for this protein was originally called C;Complex: homotetramer [validated, MUID:93267645]
C;Function:
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A;Residues: 1-467 <BLAT>
A;Cross-references: GB:AE000256; GB:U00096; NID:g1787888;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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A,TTitle: The complete genome sequence of Est A; Effective recomplete sequence of Est A; Reference number: A64720; MUID:97426617; A; Accession: E64917
A; Status: preliminary; nucleic acid sequence recomplete recom
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A; Residues: 1-15 <WEA>
R; Blattner, F.R.; Plunkett III, G.;
A; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-467 <HAY>
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A; Accession: E90918
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A;Title: Purification and crystallization of fumarase C
A;Reference number: 833825; MUID:93267645; PMID:8496960
A;Accession: S33825
                                                                                                                                                                                                                                                                                  A;Cross-references: GB:BA000007; PIDN:BAB35740.1; PID:g13361784; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Score 39; DB Pred. No. 35; 2; Mismatches
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7; PMID:9278503
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Shinagawa, H.
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Attle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: ABOS02; MUID:21534947; PMID:11677608
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Accession: B85767
Search completed: November 26, 2003, 12:36:03 Job time : 14.0602 secs
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A; Residues: 1-467 < PAR>
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A;Cross-references: GB:AE005174; NID:g12515592; PIDN:AAG56598.1; GSPDB:GN00145; UWGP:Z2:
A;Experimental source: strain O157:H7, substrain EDL933
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ller, L.; Grotbeck, E.J.; Davis, N.W.; Llm, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
lature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.;Reference number: A85480; MUID:21074935; PMID:11206551;Accession: B85767
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QBiem9 plasmodium	Q9pn44 campylobact	O97243 plasmodium		Q9lim6 arabidopsis	O81510 arabidopsis	Q8dfb6 vibrio vuln	Q53251 rickettsia	Q53246 rickettsia		<ul> <li>Q9m104 arabidopsis</li> </ul>	Q9f5v0 escherichia	Q9etx0 escherichia	Q8rnv3 escherichia	œ			Q9wta5 escherichia	Q8ihl0 dictyosteli		Q9n4b9 caenorhabdi		ש	Q9iv20 human rotav		Q8g7d1 bifidobacte		Q8x769 escherichia	. Q8zp17 salmonella

## ALIGNMENTS

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Query Match
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076447; PREVININARY; PRT; 1475 AA.
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 166.8 kDa protein.
ZK1055.1
                                             "Direct Submission."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases." EMBL, AF068721; AAC19259.1; WormPep; ZK1055.1; CE18470.
Hypothetical protein.
SEQUENCE 1475 AA; 166762 MW; 0483113C3D5D8769 CRC64;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Geisel C., Bradshaw H.;
"The sequence of C. elegans cosmid ZK1055.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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Score 43;
DB 5;
Length 1475
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF02190
Hypothetical
SEQUENCE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9KPR3;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=El Tor N19961 / Serotype 01;

MEDLINE=20406833, PubMed=10952301;

Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000
01-MAR-2003
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical VC2303.
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                                                                                                                                                                     STRAIN=0157:H7
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                           Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 406:477-483(2000).
EMBL; AE004301; AAF95447.1;
TIGR; VC2303; -.
                                                                                                                                 STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                             Escherichia
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                                                                                                                                                                                            FROM N.A.
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                                                                                                                                                                                                                                                                                                    ia coli 0157:H7.
Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003111; LON.
                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 20, (TrEMBLrel. 20, (TrEMBLrel. 21, l protein z3945.
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                                                                                                                                                                                                                                                                           teria; Gammaproteobacteria; Enterobacteriales; Escherichia.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
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D7CB416078B71A15 CRC64;
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ID Q8X3
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Best Local S
Matches 7
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Best Local S
Matches 7
  SEQUENCE FROM N.A
STRAIN=sgo49692;
Mansfield K.G., L
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Q8X3D8;
Q1-MAR-2002
Q1-MAR-2002
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Bacteria; Proteobacteria;
                                                                                                                                       Bacteria; Proteobacteria;
Enterobacteriaceae; Esche
                                                                                                                                                                                            Escherichia coli
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STRAIN=0157:H7 / R
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                                                                                                        NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
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        K. -C.,
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63.6%;
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Pred. No.
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MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T. Iida-T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
EMBL; AP002562; BAB36935.1; -
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EMBL; AE005493; AA657757.1; -.

InterPro; IPR002104; Phage_integrase.
Pfam; PF00589; PRage_integrase; 1.

Hypothetical protein; Complete protecome.

SEQUENCE 347 AA; 40506 MW; 3E5250026F2E5963 CRC64;
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specific recombinase.
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Q933W6;
01-DEC-2001
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                                                    Blank T.E., Zhong H., Bell A.L., Whittam T.S., "Molecular Variation among Type IV Pilin (bfpA) Enteropathogenic Escherichia coli Strains.";
                                                                                                       SEQUENCE FROM N.A.
STRAIN-Stoke W, 009-2710820, 2309-
MEDLINE-20536453; PubMed-11083828;
                                                                                                                                                                                Escherichia coli.
Bacteria, Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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"Molecular Variation among Type IV Pilin (bfpA)
Enteropathogenic Escherichia coll Strains.";
Infect. Immun. 68:7028-7038(2000).
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STRAIN=HSP19/4;
MEDLINE=20536453; PubMed=11083828;
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   SEQUENCE
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"Molecular Variation among Type IV Pilin (bfpA) Genes fro
Enteropathogenic Escherichia coli Strains.";
Infect. Immun. 68:7028-7038(2000).
EMBL; AR304484; AAG16272.1; -
EMBL; AR304468; AAG16256.1; -
EMBL; AR304470; AAG16258.1; -
EMBL; AR304471; AAG16258.1; -
EMBL; AR304472; AAG16260.1; -
EMBL; AR304472; FAG16250.1; -
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EMBL; AF304465; AAG16273.1; --
EMBL; AF304473; AAG16257.1; --
EMBL; AF304477; AAG16257.1; --
EMBL; AF304477; AAG16265.1; --
EMBL; AF304483; AAG16251.1; --
EMBL; AF304483; AAG16271.1; --
EMBL; AF3044946; BAA84838.1; --
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MEDLINE=20536453; PubMed=11083828;
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Q9F5U7;
01-MAR-2001
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Blank T.E., Zhong H., Bell A.L., Whittam T.S., I
"Molecular Variation among Type IV Pilin (bfpA)
Enteropathogenic Escherichia coli Strains.";
Infect. Immun. 68:7028-7038(2000).
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EMBL; AF304471; AAG16259.1; -.
InterPro; IPR001120; Prook N methyltn.
PROSITE; PS00409; PROKAR NTER METHYL; 1.
SEQUENCE 195 AA; 20329 MW; BD848F6FE
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InterPro; IPRO01120; Prok N methyltn.
PROSITE; PS00409; PROKAR NTER METHYL; 1.
SEQUENCE 195 AA; 20307 MW; BBC4C71310079F12 CRC64;
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STRAIN=012-050982;
Methanobacteriaceae;
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Archaea; Euryarchaeota; Methanobacteria;
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EMBL; AL646083; CAD18430.1; -...
InterPro; IPR00367; Fummarate_lyase.
InterPro; IPR005677; Fum hydII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S. Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Arlat M., Choisne N., Claudel-Renard C., Cunnac S., Demang Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex
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FUMC OR RSP1279 OR RS05324.
Ralstonia solanacearum (Pseudomonas
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                                                                                            Similarity 7; Conser
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                                            SDSNMNMNEL
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58.3%;
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Last annotation update)
class II (Fumarase) pro
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Pred.
                                                                                       Score 39; DB 16;
Pred. No. 1.2e+02;
2; Mismatches 1
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                         STRAIN=MC58 / Serogroup B;

MEDLINE=20175755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peders J.F., Dodson R.J.,

Nolson W.C., Gwinn M.L., DeBoy R., Petcarson J.D., Hickey E.K.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark B.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisseria meningitidis serogroup B strain

"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JYR9
Q9JYR9,
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Fumarate hydratase, class II.
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InterPro; IRR005677; Pum hydII.
Pfam; PF00206; lyase.
PRINTS; PR00149; PUMRATELYASE.
TIGRPAMS; TIGR00979; FumC_II; 1.
PROSITE; PS00163; FUMARATE_LYASES; 1
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STRAIN=C-125 / JCM 9153;
MEDLINE=0512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Se
Puji F., Hirama C., Nakamura Y., Ogasawara N.,
Horikoshi K.;
Science 287:1809-1815(2000).
EMBL; AE002495; AAP41817.1;
HSSP; P08417; 1YFM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Bacteria; Firmicutes;
NCBI_TaxID=86665;
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Last annotation update)
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Pred. No.
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time

completed: November 26, me : 31.3494 secs

2003, 12:34:35

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Q9JTR0;
01-OCT-2000
01-OCT-2000
01-OCT-2002
                                                                                                           Lyase; Co
SEQUENCE
                                                                                                                                                                                                                                                           Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
                                                                                                                                                                                                                                                                                      Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Klee S.R., Davis P., Devlin K., Petchell T., Hamlin N., Holroyd Davies R.M., Davis P., Devlin K., Petchell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR, NMB1458; -.
InterPro; IPR00362; Fummarate_lyase.
InterPro; IPR005677; Fum hydIT.
Pfam; PF00206; lyase 1; I.
PRINTS; PR00149; FUNRATELYASE.
TIGRRAMS; TIGR00979; fumC II; 1.
PROSITE; PS00163; FUMARATE_LYASES; 1.
                                                                                                                      TIGREAMS; TIGR00979; fumC II; 1. proSITE; pS00163; FUMARATE_LYASES; 1. Lyase; Complete proteome.
                                                                                                                                                 InterPro; IPR000362; Fumarate_lyase.
InterPro; IPR005677; Fum_hydII.
Pfam; PF00206; lyase_1; I.
PRINTS; PR00149; FUMRATELYASE.
TIGREAMs; TIGR00979; fumC_II; 1.
                                                                                                                                                                                                                   Nature 404:502-506(2000).
EMBL; AL162756; CAB84898.1;
HSSP; P05042; 1FUR.
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Z2491 / Serogroup A / Serotype 4A, MEDLINE=20222556; PubMed=10761919;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2002 (TrEMBLrel. 22,
Fumarate hydratase class II
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Last annotation update)
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                                                                 Score 39; DB 16;
Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
2; Mismatches 1
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                                                                                                           6F63B3D506E26C85 CRC64;
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Perfect score:
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             Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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2 US-10-092-138-14
2 US-09-230-111C-14
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5 US-10-106-698-4719
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1 US-09-955-999-91
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Sequence 16, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 4719, Appl
Sequence 91, Appl
Sequence 91, Appl
Sequence 168, App
Sequence 1111, App
Sequence 1111, App
Sequence 114, App
Sequence 114, App
Sequence 144, App
Sequence 145, App
Sequence 144, App
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ALIGNMENTS

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US-08-681-219-16
Sequence 16, Application US/08681219
Publication No. US20020058607A1
GENERAL INFORMATION:
APPLICANT: Takaski Sato and Junn Yanagisawa
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GIGF
THERESEE COOPER & DUNDAIN LLP
STREET: 1185 AVENUE OF THE AMERICAS
CLIY: NOW YORK
COUNTRY: U.S.A.
ZIP: 10036
COUNTRY: U.S.A.
ZIP: 100

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                                                                                                          ; OTHER INFORMATION: Description of Artificial ; OTHER INFORMATION: Sequence:source:synthesized US-09-230-111C-14
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                                Query Match

Best Local Similarity 100.

Matches 15; Conservative
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APPLICANT: Sato, Taka-Aki
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: 65823/JPW/PT
CURRENT APPLICATION NUMBER: US/10/092,138
CURRENT APPLICATION NUMBER: US/10/092,138
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Publication No. US20030203414A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yanagisawa, Junn
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOMAIN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, J
                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 48962-A-PCT-US
                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:source:synthesized
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ORGANISM: Artificial Sequence
FEATURE:
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1 PPTCSQANSGRISTL 15
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Pred. No.
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Pred. No.
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Pred. No.
                                         Mismatches
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US-09-764-868-1068
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US-10-106-698-4719
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                                                           Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1068
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698.
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 3.0
                                                                                                                                                                                       NAME/KEY: SITE LOCATION: (46) OTHER INFORMATION:
                                                                                                                                                                                                                                     LOCATION: (30)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                    ORGANISM: Homo
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; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring US-09-955-999-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-106-698-6252
                                                                                    FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (126)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
5-10-106-698-6252
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  Query Match 50.6%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local
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CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 60/234,997
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
1EQ ID NO 91
                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR TILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypepti
TITLE OF INVENTION: Antibodies, and Methods Based Thereon
FILE REFERENCE: PT086P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Barash et al
                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 13
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
LOCATION: (46)
COTHER INFORMATION: Xaa equals any of the naturally occurring
                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                        LENGTH: 126
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
LOCATION: (30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133
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Similarity 77.8%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPTCSQANS 9
; Score 40; DB;
; Pred. No. 75;
2; Mismatches

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
                                           15; Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 133;
  Indels
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  Gaps
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US-09-925-302-768
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                                                   . NAME/KBY: SITE
. LOCATION: (80)
. OTHER INFORMATION: Xaa equals any of the naturally occurring
US-09-925-300-1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-925-300-1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Xaa equals any of the naturally occurring US-09-925-302-768
                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 768, Application Patent No. US20020044941A1
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1118, Application US/09925300 Patent No. US20020151681A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
LOCATION: (6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PA104
                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                         LOCATION: (45)
OTHER INFORMATION:
                                                                                                                                                           NAME/KEY: SITE
                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 404
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6; Conserv
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                                                                                                                        Xaa
 49.4%;
58.3%;
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                                                                                                                      equals
Score 39;
Pred. No.
                                                                                                                        any of the naturally occurring
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Pred. No. 2.4e+02;
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 69;
                                                                                                                                                                                                                                                                                                                                                                                                                               and Antibodies
                  10;
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                  Length 80;
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                                                                                                                           L-amino
                                                                      L-amino acids
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11117
LENGTH: 161
TYPE: PRT
ROANISM: Streptomyces avermitilis
US-10-156-761-11117
                                                                                                                 ; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                         APPLICANT: CAENEFEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
CURRENT FILING DATE: 2001-06-26
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Best Local Similarity 5/...
Conservative
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                                       Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 114, Application US/09888615 Patent No. US20020064856A1
                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JF 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262 CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PLOWMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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       1 PPTCSQANSGRISTL 15
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                           Conservative
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                                                          49.4%;
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                                                            Score 39; DB 9;
Pred. No. 3.1e+02;
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Pred. No. 1.
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                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 161;
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                                         5; Indels
                                                                           Length 359;
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                                         Gaps
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RESULT 14
US-09-771-161A-235
; Sequence 235, Application US/09771161A
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US-09-771-161A-144
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US-09-771-161A-145
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR PPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 145, Application US/09771161A
PATENT NO. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
                                                                                                                                                                                                                                                                                            SEQ ID NO 144
LENGTH: 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 144, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS Of PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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SEQ ID NO 145
                                                                                                                                                                       Matches
                                                                                                                                                                                                       Query Match
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                     Local Similarity nes 7; Conservat
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les 7; Conserva
                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 PTCSATNLSRVAGL 131
                                                                                                                                  2 PTCSQANSGRISTL 15
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                                                                                                PTCSATNLSRVAGL 131
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                                                                                                                                                                                        49.4%;
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                                                                                                                                                                     Score 39; DB 10; Pred. No. 6.6e+02; 2; Mismatches 5;
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Pred. No. 3.4e+02;
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                                                                                                                                                                                                       Length 780;
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GENERAL INFORMATION:

APPLICANT: LEVINE, et al.

APPLICANT: LEVINE, et al.

TITLE OP INVENTION: VARIANTS OF PROTEIN KINASES

FILE REFERENCE: 802630-2005.1

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 09/724,676

PRIOR APPLICATION NUMBER: 13676

PRIOR APPLICATION NUMBER: 13676

PRIOR PILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 135619

PRIOR APPLICATION NUMBER: 135619

PRIOR APPLICATION NUMBER: 135619

PRIOR APPLICATION NUMBER: 300-04-12

NUMBER OF SEQ ID NOS: 273

SOFTWARE: PAT DNOS: 273

SOFTWARE: PAT DNOS: 273

CORGANISM: Homo sapiens

US-09-771-161A-235
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 273
SOPTWARE: PatentIn version 3.0
SEQ ID NO 236
LENGTH: 942
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LEVINE, et al.
TITUE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCES: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-15-56
PRIOR APPLICATION NUMBER: 13676
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
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Search completed: November 26, 2003, 12:38:39 Job time: 27.1084 secs
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US-09-771-161A-236
                                                                                                                                                                                                     Query Match 49.4%; Score 39; DB 10; Length 942; Best Local Similarity 50.0%; Pred. No. 8e+02; Matches 7; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 49.4%; Score 39; DB 10 Best Local Similarity 50.0%; Pred. No. 8e+02; Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 236, Application US/09771161A Patent No. US20020110811A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PACENT NO. US20020110811A1 GENERAL INFORMATION:
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118 PTCSATNLSRVAGL 131
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 2000000000
     A Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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Match Length DB
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                                                                 AAW50175
AAU86416
AAU86429
ABG29167
AAW43449
ABG02424
AAG73945
AAU44755
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                 Signal-transducing
Androgen receptor
Androgen receptor
Androgen receptor
Novel human diagno
Propionibacterium
Tobacco laccase cl
Novel human diagno
Human colon cancer
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123	123	94	92	92	92	78	239	108	80T.	1257	1074	1074	942	941	940	939	939	542	542	359	222	153	117	104	92	80	72	748	557	404	404	126	4	144	
17	17	22	22	22	20	22	22	23	21	20	22	22	19	21	22	22	22	22	22	23	21	21	21	22	22	21	22	22	19	22	21	22	22	22	22
AAR94713	AAR94712	AAG74950	AAM84735	AAU04456	AAW99896	ABG27485	ABG27685	ABP00490	AAB40463	AAY06427	ABG10255	ABG07890	AAW56699	AAY94737	ABG07054	ABG14439 ·	ABG12508	AAB61791	AAB61779	AAU82756	AAG44730	AAY71106	AAY70526	ABG04821	AAU41900	AAB56540	AAU61904	ABB60412	AAW43448		AAB58430	7	165	AAM39866	AAU17503
PRRSV ISU-22 nucle	PRRSV ISU-1894 nuc	Human colon cancer		Human u-PAR extrac	nase-ty	Novel human diagno	human		-			Novel human diagno	μ.		man		œ	Sunflower berberin	wer b	0	Zea mays protein f	Human Hydrolase pr		Novel human diagno	Propionibacterium	Human prostate can	Propionibacterium	la melar	ດ	n polypeptide	cancer		_	Human polypeptide	Novel signal trans

## ALIGNMENTS

AAW50175 standard; peptide; 15

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RESULT 1
AAW50175
ID AAW5
XX
AC AAW5
AC AAW5
XX
XX
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XX
   PT XXXX
Inhibition of signal transduction - by inhibiting binding between a signal-transducing protein and a cytoplasmic protein, for treating
                                                                                                                                                                                                      Inhibition; specific binding; signal-transducing protein; cytoplasmic protein; proliferation; cancer cell; apoptosis; virally infected cell.
                                 WPI; 1998-145347/13.
                                                                                                                                                              WO9805347-A1.
                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                  Signal-transducing protein carboxy-terminal peptide
                                                                                                                                                                                                                                                                                              AAW50175;
                                                  (UYCO ) UNIV COLUMBIA NEW YORK.
Sato T, Yanagisawa J;
                                                                                               22-JUL-1996;
                                                                                                                                          12-FEB-1998
                                                                                                                                                                                                                                                                       16-JUL-1998
                                                                                                                     18-JUL-1997;
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                                                                                               96US-0681219.
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Propionibacterium

e.g. cancer or viral infection

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RESULT 2
AAU86416
FXGXCCCCCCXXX
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Matches
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                                         The invention relates to identifying a binding peptide which binds a receptor and which is a member of a combinatorial library of peptides, comprising screening a combinatorial peptide library presented in the form of cells which coexpress the receptor or its ligand-binding receptor moiety and one member of the library, together with a signal producing system for reporting binding of the peptide to the receptor. Also included is a method for predicting the receptor-modulating activity of a compound which modulates the biological activity of a receptor comprising (a) identifying peptides which bind the receptor by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   any amino acid (e.g. the present peptide), and a cytoplasmic protein (CP) containing the sequence AAW50162 or AAW50163. The composition can be used to inhibit the proliferation of cancer or virally infected cells, or induce apoptosis in cancer or virally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel composition is capable of inhibiting specific binding between a signal-transducing protein (STP) having the between terminal sequence (Ser/Thr)-taa-(Val/Ile/Leu), where carboxy-terminal sequence (Ser/Thr)-taa-(Val/Ile/Leu), where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Androgen receptor; breast can receptor modulating compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU86416 standard; Peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17;
                                                                                                                                                                                                                                                    Identifying receptor-binding peptides comprises screening combinatorial peptide library presented in form of cells each of which coexpress one peptide member and receptor with signal producing system for reporting
                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-2000; 2000US-0614865
21-MAY-2001; 2001US-0860688
                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2001; 2001WO-US21867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200204956-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Androgen receptor binding peptide B8H3.
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                               method above,
                                                                                                                                                                                                          Example 502; Page 154; 175pp; English.
                                                                                                                                                                                                                                                                                                                      WPI; 2002-154969/20
                                                                                                                                                                                                                                                                                                                                                     Fowlkes DM,
                                                                                                                                                                                                                                         peptide member
binding
                                                                                                                                                                                                                                                                                                                                                                                   (KARO-) KARO BIO USA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor; breast cancer; combinatorial peptide library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page
ve, (b) using a number of the peptides to predict the receptor-
activity of a compound by (i) providing a panel of
peptides, where the members differ in their ability to bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 AA;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide which binds a vertebrate, mammalian, preferably human receptor, can intracellular, nuclear, oestrogen or androgen receptor. The identified peptides which bind to the receptor are useful for predicting the receptor-modulating activity of a compound (e.g. ant/agonists). The receptor-binding library members are useful in the prediction of the cability of small organic molecules, suitable for pharmaceutical use cability of small organic molecules, suitable for pharmaceutical use cability of oestrogen receptors, for breast cancer treatment), to interact with the receptor. The analyte-binding molecules can also be used for in vivo imaging. The method has several advantages over whole canimal-based assay systems in that the same technology can be applied to a variety of different receptors, the system can be used for high throughput screening and compound characterisation, and gives very constituted the system of receptor activity using very much less protein. The present sequence is an androgen receptor binding peptide from a combinatorial peptide library.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the receptor depending on reference conformations the receptor in, where the effect of a number of reference substances known to modulate the biological activity of the receptor on the binding of member of the panel is known and is characterised as a reference
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                     Androgen receptor; breast cancer; combinatorial peptide library; receptor modulating compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Androgen receptor binding peptide B8H3.
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                                                                                                                                                                                                           12-JUL-2000; 2000US-0614865
21-MAY-2001; 2001US-0860688
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                                                                                                                                                                                                                                                                                                                                               WO200204956-A2
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                                                                                                                                                                                                                                                                                                           17-JAN-2002
                                                                                                                                                                       (KARO-) KARO
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                                                                                           2002-154969/20
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                                                                                                                                 DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                 Barnett
                                                                                                                                                                       BIO USA
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                                                                                                                                 Buehrer
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Identifying receptor-binding peptides comprises screening combinatorial peptide library presented in form of cells each of which coexpress one peptide member and receptor with signal producing system for reporting binding

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RESULT 4
ABG29167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C comprising screening a combinatorial peptide which comprising screening a combinatorial peptide (ibrary presented in the C comprising screening a combinatorial peptide (ibrary presented in the C comprising screening a combinatorial peptide (ibrary presented in the C compound which modulates the biological activity of a receptor c compound which modulates the biological activity of a receptor c compound which modulates the biological activity of a receptor c compound which modulates the biological activity of a receptor computating (a) identifying peptides which bind the receptor by the compound which modulates the biological activity of a receptor computating activity of a compound by (i) providing a panel of c the receptor is now the receptor defect of a compound by (i) providing a panel of c in, where the effect of a number of reference substances known to modulate the biological activity of the receptor on the binding of each member of the panel is known and is characterised as a reference of ingerprint for each reference substance, (ii) gereening a test substance fingerprints and (iv) predicting the cest fingerprint to the receptor to determine its effect on the binding of each member of the panel to the receptor, thereby the binding of each member of the panel to the receptor, thereby the binding at test fingerprint for the test substance, (iii) gereening a test substance with a set of particle which binds a vertebrate, mammalian, preferably human receptor, can intracellular, nuclear, oestrogen or androgen receptor. The identified peptides which binds a vertebrate, mammalian, preferably human receptor, can intracellular, nuclear, oestrogen or androgen receptor. The identified peptides which binds to the receptor are useful for predicting the receptor-modulating activity of a compound (e.g. ant/agonists).

The receptor-binding library members are useful for predicting the receptor binding the receptor activity of small organic molecules, suitable for pharmaceutical use of other condities of the sevent adv
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Matches
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                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                    Novel human
                                                                                                                                                                                                                          13-FEB-2002
                                                                                                                                                                                                                                                                                                  ABG29167 standard; Protein; 1082 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to identifying a binding peptide which binds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 TCSQANSGRIS 13
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                                                                                                                                                                                  diagnostic protein #29158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                      (first entry)
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0.074;
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RESULT 5
AAU63049
ID AAU6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical cimaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations conditions for genetic disorders or other traits to assess biodiversity amino acid sequences of the invention.

CC and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed car for who, which label for generates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
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                                                                                                                                                             SAPHO syndrome; synovitis; acne; uveitis; endophthalmitis; bone;
                                                                                                                                                                                                                    Propionibacterium acnes immunogenic protein #23945
                                                                                                                                                                                                                                                                                                                                 AAU63049 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 59526; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation
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23-AUG-2000;
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                                                                                                                                                                                                                                                         27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                            uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                             379 PPDCGGANPGGIST 392
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9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPTCSOANSGRIST 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1082 AA;
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2000US-0649167.
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to isolated polynucleotide (I) and
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Pred. No. 99;
0; Mismatches
                                                                                                                                                               pustulosis; hypertosis; osteomyelitis;
joint; central nervous system; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1082;
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Propionibacterium

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Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fifty.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
30-MAY-1997;
                                                                                                           Nicotiana tabacum
                                                                                                                                                        Tobacco; laccase; oxidoreductase; probe; hybridisation; sycamore; transgenic plant; digestibility; forage crop; paper manufacture;
                                                                                                                                                                                                                                            01-JUN-1998
                                                                                                                                                                                                                                                                                                           AAW43449 standard; Protein; 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW, Persing DH, L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001WO-US12865
                                            04-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID No 24244; 1069pp; English
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                                                                                                                                          parasite
                                                                                                                                                                                                          laccase clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
           97WO-FR00948.
                                                                                                                                            resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.7%;
42.9%;
                                                                                                                                                                                                          pTL-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
17;
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RESULT 7
ABG02424
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diphenols) encoded by the partial length clone pTL-2. The sequence is lacking part of the C-terminus of the protein. The gene sequence we isolated from a cDNA library from tobacco leaves using a probe derived from the sequence of the sycamore (Acer pseudoplantanus) laccase gene. The gene can be used to transform plant cells for producing transgenic plants having a reduced or altered lighin content, for improved digestibility of forage crops, for paper manufacture. Plants with increased lighin content may have better resistance to parasites.
          New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to assebiodiversity -
                                                                                                                                                                                 31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying lignin biosynthesis in planmRNA - or its anti-sense complement, fodder and for paper production
                                                                                  N-PSDB; AAS66611.
                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                        11-OCT-2001.
                                                                                                                                                                                                                                                                                   WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #2415
                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG02424 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a tobacco laccase (an oxidoreductase acting diphenols) encoded by the partial length clone pTL-2. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 19; Page 37-39; 72pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-032655/03.
N-PSDB; AAV01597.
                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG02424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-1996;
                                                                                                                                                      (HYSE-)
                                                                                                 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%;
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Pred. No. 79;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 409
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                            to assess
                                          mutations
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RESULT 8
AAG73945
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CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO or format directly from WIPO.
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Matches 10
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), wher
                                                                                     Claim 11;
                                                                                                                                                                                                                                WPI; 2001-235357/24.
N-PSDB; AAH33376.
                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-1999;
03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human colon cancer antigen protein SEQ ID NO:4709
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                                                                                                                                                                     Nucleic acids encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; colon cancer; colon cancer antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG73945 standard; Protein; 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 32783; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                          preventing,
                                                                                                                                                                                                                                                                                                                  Barash SC,
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99US-0163280.
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                                                                               9803pp;
                                                                                                                                       4277 human
diagnosing
                                                                                                                                                                                                                                                                                                                  Birse CE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,
                                                                                  English
                                                                                                                                          colon c
                                                                                                                                                                                                                                                                                                                  Rosen CA;
                                                                                                                                    cancer-associated polypeptides, r treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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밁 Ś

Sequences AAU39105-AAU68017 represent Propionibacterium acnes polypeptides. The proteins and their associated DNA sequences the treatment, prevention and diagnosis of medical conditions

are used in

Example 1; SEQ ID No 5950; 1069pp; English.

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RESULT 9
AAU44755
IID AAU44755
AC AAU44755
AC AAU4
AC 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                  Propionibacterium acnes polypeptides and nucleic acids useful vaccinating against and diagnosing infections, especially use treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                              L'maisonneuve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dermatological; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein #5651.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                          2001-616774/71.
DB; AAS59524.
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                                                                                                                                                                                                                                                                                                                                                                        Persing DH, I
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63.6%;
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, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                   infections, especially useful
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RESULT 10
AAU17503
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Best Local S
Matches 8
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
17-MAX-2000;
19-MAX-2000;
07-JUN-2000;
28-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                    17-JAN-2001; 2001WO-US01312
                                                                                                                                                                                                                                                                                                                                      02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                         WO200154733-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel signal transduction pathway protein, Seq ID 1068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU17503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
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                2000US-0190076.
2000US-0198123.
2000US-0205115.
2000US-0209467.
2000US-0214886.
2000US-0215185.
2000US-0216647.
2000US-0216880.
2000US-0217496.
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; 2000US-0186350.
; 2000US-0189874.
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57.1%;
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23-AUG-2000
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08-SEP-2000
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26-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                    2000US-0241786.

2000US-0241787.

2000US-0241808.

2000US-0241809.

2000US-0241826.

2000US-0244617.
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2000US-0239935.
2000US-0239937.
2000US-0240960.
2000US-0241221.
2000US-0241785.
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2000US-0235836.
2000US-0236327.
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2000US-0236802.
2000US-0237037.
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2000US-0234274.
2000US-0234997.
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2000US-0231413.
2000US-0231414.
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2000US-0231242.
2000US-0231243.
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2000US-0229509.
2000US-0229513.
2000US-0230437.
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2000US-0229964.

2000US-0224518.

2000US-0224519.

2000US-0225213.

2000US-0225213.

2000US-0225214.

2000US-02252667.
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2000US-0232081.
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2000US-0229344.
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2000US-0232397.
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2000US-0229287
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2000US-0227182.
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05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
    The invention relates to novel isolated polypeptides (I), and polynucleotides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis (), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell annemia), myeloproliferative disorders, primary haematopoletic disorders, hyperproliferative disorders (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g. Gaucher's disease and cancer), neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                              Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immudisorders and neuronal disorders -
                                                                                                                                     Claim 1; SEQ ID No 1068; 880pp; English.
                                                                                                                                                                                                                                               Rosen
                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME
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DB; AAS27420.
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2000US-0251479.
2000US-0251856.
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2000US-0249299.
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immune

The invention relates to human nucleic acids the encoded polypeptides (AAM38642-AAM42213) immunosuppressant and cytostatic activity. The

and cytostatic activity. The polynucleotides are useful

with

(AAI57798-AAI61369)

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RESULT 11
AAM39866
ID AAM39
XX AAM39
XX AAM39
XX AAM39
XX AAM39
XX Human
XX Human
XX Human
XX Human
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Best Local :
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14-SEP-2000;
19-OCT-2000;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
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                                                                                                                                                                                                         WPI; 2001-442253/47.
N-PSDB; AAI59022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-2000;
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Zhou
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                                                                                         SEQ ID
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317.
2000US-0598042.
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Wehrman T, X
Goodrich R,
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                                                                                       3011; 10078pp; English.
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77.8%;
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Xu C, Xue
R, Drmanac
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Pred. No.
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Zhang J;
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AAM41652
ID AAM4
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Best Local S
Matches 7
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Wang
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilization of the activities such as: Immune system suppression, activities the activities such as: Immune system suppression,
                                                                                                                                         Zhao
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 Example
                                 Novel nucleic acids such as central nerv
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                                                                                                                                                                                                                                               29-NOV-2000;
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                                                                                       2001-442253/47.
DB; AAI60808.
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Wang Z,
Zhou P,
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 SEQ
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; 2000US-0598042.
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2000US-
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                                   nervous
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Wehrman T,
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3-0727344.
                                                                                                                                         Goodrich
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6583; 10078pp; English
                                 polypeptides, us
system injuries
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Pred. No. 84;
1; Mismatches
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Xu C,
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Xue
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Yang
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Zhang
                                                     disorders
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                                                                                                                                                                         Wang D;
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Best Local S
Matches 7
AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletion in a patient's genome that affect the activity of P by expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activity. Inhibit activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.N.S
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                                                                                                                                                                                                           Nucleic
                                                                                                                                                                                                                                                                                       Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein SEQ ID NO:6242.
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                                                                                                                                                                                          c acids encoding for preventing,
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and/or treating colorectal cancers -
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Best Local &
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                                            Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                       antigens, userui roz
such as lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; lung cancer associated protein; neuroprotective; cytostatic; cardioactive, immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; prollferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                        Claim 11;
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N.B. Pages 666 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bung
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DB; AAF18306.
                                                                                                                                                                                                                                                                                                                                                                                                                        cancer associated gene sequences, referred gene, useful for treatment, prevention, and
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
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                                                                                                                                                                                                        Novel nucleic acids and such as central nervous
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N-PSDB; AAI59780.
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09-JUL-2000;
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CC localised neuropathies and central nervous system diseases, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activities such as: Immune system suppression, CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC Note: The sequence data for this patent did not form part of the printed CC specification.

XX Sequence 404 AA;

Query Match 50.6%; Score 40; DB 22; Length 404; Best Local Similarity 50.0%; pred. No. 3.4e+02; Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0; Length Local Similarity 20.0%; pred. No. 3.4e+02; DB 1 pprcpanscr 22

Search completed: November 26, 2003, 12:30:25

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48 C: 78 C: 225 PC 52907 MW;

C2H2-TYPE 1. C2H2-TYPE 2. POLY-SER.

4A5F3EA3603B17C3 CRC64;

Conservative

50.6%; Score 40; DB 1; Length 474; 60.0%; Pred. No. 19; tive 0; Mismatches 6; Indels

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EMBL; Z50017; CAA90320.1;  PIR; S66480; S66480.  HSSP; P08047; 1SP2.  InterPro; IPR007087; Znf_C2H2.  Pfam; PF00096; Zf_C2H2; 2.  ProDom; PD000003; Znf_C2H2; 2.  SMART; SM00055; ZnF_C2H2; 2.  PROSITE; PS00028; ZINC_FINGER_C2  PROSITE; PS50157; ZINC_FINGER_C2  Transcription regulation; Repres  Zinc_finger; Metal-binding; Repres	-i- SIMILI -i- SIMILI -i- SIMILI -i- SIMILI This SWIS; between the Europ use by a modified entities or send a	SEQUEN STRAIN MEDLIN Cassax "The y and fu FEBS fu FEBS fu	ULT 1 1 KLULA 1 KLULA P50898; 01-OCT-1996 01-OCT-2001 Regulatory F MIG1. Kluyveromyce Bukaryota; E Saccharomyce	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
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Protein kinase C-like 1 (EC 2.7.1.-) (
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PROSITE;
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"Amino acid sequences of alpha-helical segments from S-
carboxymethylkerateine-A. Complete sequence of a type-II segment."
Biochem. J. 173:865-371(1978).

-i- FUNCTION: WOOL MICROFIBRILLAR KERATIN.
-i- FUNCTION: WOOL MICROFIBRILLAR KERATIN SOF CYTOSKELETAL AND
MICROFIBRILLAR KERATIN, I AND II (40-55 AND 56-70 KILODALTONS,
RESPECTIVELY). AT LEAST ONE TYPE OF CYTOSKELETAL KERATIN IS
SEQUENCE FROM N.A.
MEDLINE=95080426; PubMed=7988719;
Palmer R.H., Ridden J., Parker P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Keratin, type II microfibrillar (Low-sulfur keratin) (Fragment).
                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                              NAMOH
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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21-JUL-1986
                                                                                         Homo sapiens (Human)
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InterPro; IPR003054; Keratin_II.
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Crewther W.G., Inglis A.S., McKe
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Primates;
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           Parker P.J.;
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R -> K.
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Pred. No.
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ProDom; PD000001; F...

R SMART; SM00023; CZ; 1.

DR SMART; SM00023; S_TKX; 1.

DR SMART; SM00133; S_TKX; 1.

DR SMART; SM00103; S_TKC; 1.

DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.

DR PROSITE; PS00118; PROTEIN KINASE_DOM; 1.

DR PROSITE; PS0011; PROTEIN KINASE_DOM; 1.

PROSITE; PS0001; PROTEIN KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN KINASE_NOM; 1.

PROTEIN KINASE_STIMP CHORDER CONTINUES.

PROMAIN

615 874 PROMAIN STAND 614 644 ATP (BY SIMILARITY).

644 644 ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                             "A novel protein kinase with leucine zipper-like sequences: i catalytic domain is highly homologous to that of protein kina Biochem. Biophys. Res. Commun. 19:897-904(1994).

11 FUNCTION: CAN PHOSPHORYLATE RIBOSOMAL PROTEIN S6. MEDIATE RHO DEPENDENT INTRACELLULAR SIGNALLING (BY SIMILARITY).

12 ENZYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARD AND TO A LESSER EXTENT BY OTHER ACIDIC PHOSPHOLIPIDS (BY SIMILARITY).

13 SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

14 SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

15 SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

16 SUBCELLULAR LOCATION: MUSCLE, KIDNEY, AND PANCREAS.

17 PIN: AUTOPHOSPHORYLATED; PREFERABLY IN SERINE.

18 PIM: AUTOPHOSPHORYLATED; PREFERABLY IN SERINE.

19 PIM: AUTOPHOSPHORYLATED; PREFERABLY IN SERINE.

19 SIMILARITY; BELONGS TO THE SER/THR FAMILY OF PROTEIN KINA:
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GO; GO:0006468; P:proceein amino acid pl
GO; GO:0007165; P:signal transduction;
InterPro; IPR000008; C2:
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EMBL; S75546; AAB33345.1;
EMBL; D26181; BAA05169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palmer R.H., Ridden J., Parker P.J., "Cloning and expression patterns of kinase-C-related kinase family."; Eur. J. Biochem. 227:344-351(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=Fetal brain; PMEDLINE=95154310; P
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PDB; 1CXZ; 23-MAY-00.
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MEDLINE=94183274; F
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                                                                                                                                                                                                                                                                                                                                            InterPro;
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IPR000719; Prot_kinase.
IPR000861; REM_repeat.
IPR002290; Ser_thr_pkinase.
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en J., Parker P.J
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Sarkissian M., Winne A., Lafyatis R.;
The mammalian homolog of suppressor-of-white-apricot regulates
alternative mRNA splicing of CD45 exon 4 and fibronectin IIICS.
J. Biol. Chem. 271:31106-33114 (1996).
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                                              GO; GO:0008248; F:pre-mRNA splicing factor activity; GO; GO:0006376; F:mRNA splice site selection; TAS. InterPro; IPR00061; Surp. Pfam; PP01805; Surp; 2.

BMART; SM00648; SWAP; 2.
                                                                                                                                                                                                                                                                                                               the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                GK, Q12872
                                                                                                                                                                                                                                        EMBL; U08377; AAA19604.1; -. Genew; HGNC:10790; SFRS8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE=97094873; PubMed=8940107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denhez F., Lafyatis R.;
"Conservation of regulated alternative splicing and identification of functional domains in vertebrate homologs to the Drosophila splicing regulator, suppressor-of-white-apricot.";
J. Biol. Chem. 269:16170-16179(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TI8SUE=Placenta;
MEDLINE=94266805; PubMed=8206918;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFRS8 OR SWAP
Homo sapiens (Human)
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Splicing factor, arginine/serine-rich 8 (Suppressor of white apricot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGEN
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                                PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 271:31106-31114(1996).
FUNCTION: MAY FUNCTION AS AN ALTERNATIVE SPLICING REGULATOR.
FUNCTION: MAY FUNCTION AS AN ALTERNATIVE SPLICING REGULATOR.
REGULATE ITS OWN EXPRESSION AT THE LEVEL OF RNA PROCESSING. ALSO
REGULATES THE SPLICING OF FIBRONECTIN AND CD45 GENES. MAY ACT, A:
LEAST IN PART, BY INTERACTION WITH OTHER R/S-CONTAINING SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear (Potential). SIMILARITY: Contains 2 SURP motif repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaborationen the Swiss Institute of Bioinformatics and the EMBL outstation
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/FTId=VAR 014937.
K->R: SUBSTANTIAL REDUCTION
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RA Zylka M.J., Reppert S.M.;

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

C. I-FUNCTION: CIRCADIAN REGULATOR THAT MAY ACT AS A TRANSCRIPTION CC FACTOR. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL LOOP, DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT TRANSCRIPTIONAL INHIBITION. EXPRESSION OSCILLATES WITH A 24 HR CC RHYTHM IN THE SUPRACHIASMATIC NUCLEUS (SCN) AND THE WHOLE EYES.

CC RHYTHM IN THE SUPRACHIASMATIC NUCLEUS (SCN) AND THE WHOLE EYES.

CC OSCILLATIONS ARE MAINTAINED UNDER CONSTANT DARKNESS AND ARE COSCILLATIONS. THEE IS A 4 HOUR CC RESPONSIVE TO CHANGES OF THE LIGHT/DARK CYCLES. THERE IS A 4 HOUR CC TIME DELAY BETWEEN PERI AND PERZ OSCILLATIONS. THE EXPRESSION CC INTERPEAR TO ORIGINATE FROM RETINA.

CC INTERPEDIAL LOCATION: Nuclear (POLENLIA).

CC INTESUBACETIVE DAY. CONSTITUTIVE EXPRESSION IN SCN DURING CONTINGUES SPECIFICITY: IN THE BRAIN, HIGH EXPRESSION IN THE CORNU AMMONIS CONTINGUES OF THE HYPPOCAMPUS. ALSO EXPRESSED IN THE SUBJECTIVE DAY. CONSTITUTIVE EXPRESSION IN THE CORNU AMMONIS OF THE HYPPOCAMPUS. ALSO EXPRESSED IN THE SUBJECTIVE AND THE GLOWERULI OF THE OLFACTORY BULB, AND AT A
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Albrecht U., Sun Z.S., Bichele G., Lee C.C.;
"A differential response of two putative mammalian regulators, mperl and mper2, to light.";
Cell 91:1055-1064(1997).
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Mammalia; Eutheria;
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15-JUL-1999 (Rel. 38, Last
16-OCT-2001 (Rel. 40, Last
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Zylka M.J., Reppert S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shearman L.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9427249;
lka M.J., Weaver D.R., Kolakowski L.F. Jr.,
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Rodentia;
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Pred. No.
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MEDLINE=86168010;
                [2]
SEQUENCE FROM
                                   Wang S.-Z., Chen J.-S., Johnson J.L.;
"The presence of five nifH-like sequences in Clostridium pasteurianum: sequence divergence and transcription proponic Acids Res. 16:439-454(1988).
                                                                                SEQUENCE FROM N.A. MEDLINE=88124247; PubMed=2829127;
                                                                                                                               Clostridium pasteures;
                                                                                                                                                                                   Nitrogenase
                                                                                                                                                                                                          01-MAR-1989
                                                                                                                                                                                                                    P09552;
01-MAR-1989
                                                                                                                                                                                                                                          NIH2
                                                                                                                                                                                                                                                   CLOPA
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR001610; PAC.
InterPro; IPR001014; PAS_domain.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF036893; AAC39942.1; EMBL; AF035830; AAC53592.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
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                                                                                                               NCBI_TaxID=1501;
                                                                                                                                                              NIFH2
                                                                                                                                                                                             28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; T09493; T09493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription
                                                                                                                                                                       (Nitrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long by for this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLY NEONATAL LIFE.

INDUCTION: BY LIGHT EXPOSURE DURING SUBJECTIVE NIGHT, BUT NOT DURING SUBJECTIVE DAY.

SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
                                                                                                                                                                                                                                                                                                1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization SIMILARITY: Contains 1 PAS-associated C-terminal (PAC)
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                                                                                                                                                                                                                                         CLOPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                          Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                     PPTCSQ----ANSGRIST 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50112; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requires a license agreement
                                                                                                                                                                                                                                                                                                PPTCNEPSDTQNSDAIST
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                                                                                                                                                                                 (Rel. 10, Last & (Rel. 41, Last & rootein 2
                                                                                                                                    pasteurianum.
irmicutes; Clostridia;
                                                                                                                                                                                                                    (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                           Conservative
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     PubMed=3457003;
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                                                                                                                                                                     sequence update)
annotation update)
(EC 1.18.6.1) (Nitrogenase
(Nitrogenase reductase).
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PAS 1.

PAS 2.
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NUCLEAR
P -> S (
K -> R (
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Pred. No.
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                                                                                                                                       Clostridiales;
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76;
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••
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BUT NOT IN SKELETAL
                                                                                                                                        Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                           Indels
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                                               properties.";
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Matches 7
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P09555;
01-MAR-1989
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J. Bacteriol. 166:162-172(1986).

-i- FUNCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN FIXATION ARE CAPALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THI IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.

-i- CAPALYZIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATI = 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              Clostridium pascecce
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLOPA
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MEDIJINE-88124247; PubMed=2829127;
Wang S.-Z., Chen J.-S., Johnson J.L.;
Wang S.-Z., Chen J.-S., Johnson J.L.;
The presence of five nifH-like sequences in Clostridipasteurianum: sequence divergence and transcription proposed chaids Res. 16:439-454(1988).

IPONCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
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HAMAP; MF 00533; -; 1.
InterPro; IPR005977; NifH.
InterPro; IPR000392; NitrogenaseII.
Pfam; PF00142; fer4 NifH; 1.
PRINTS; PR00091; NITROGNASEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X07473; CAA30360.1;
EMBL; M21537; AAA83529.1;
PIR; S01724; S01724.
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          Clostridium.
                                                                                                                                                                                                                                                                                                                               NIFH6
                                                                                                                                                                                                                                                                                                                                                                           Nitrogenase
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SIMILARITY: BELONGS TO THE NIFH / BCHL / CHLL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: BINDS ONE 4FE-4S
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PS00692; NIFH_FRXC_2; 1.
PS00746; NIFH_FRXC_1; 1.
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                                                                                                                                                                                                                                                                                                                                                (Rel. 41, Last annotation update) iron protein 6 (EC 1.18.6.1) (Nitrogenase Fe protein 6) (Nitrogenase reductase).
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                                                                                                                                                                                                                                                                                                     pasteurianum.
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                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
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IRON-SULFUR (4FE-4S);
FB30D051E8B38FEC CF
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Best Local S
Matches 7
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Q03405; Q12876;
Q9UMVO;
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Q9UMVO;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Urokinase plasminogen activator surface receptor precursor (uPAR)
PAR) (Monocyte activation antigen Mo3) (CD87 antigen).
PLAUR OR UPAR OR MO3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
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HAMAP, MF 00533; -; 1.

InterPro; IPR005977; NifH.

InterPro; IPR000392; NitrogenaseII.

Pfam; PP00142; fer4 NifH; 1.

PRINTS; PR00091; NITROGNASEII.
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                                                         SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=92268511; PubMed=1316922;
Min H.Y., Semnani R., Mizukami I.F., Watt K.,
"CDNA for Mo3, a monocyte activation antigen,
                                                                                                                                                                        "Cloning and expression of the receptor plasminogen activator, a central molecul dependent proteolysis.", EMBO J. 9:467-474(1990).
                                                                                                                                                                                                                                                            MEDLINE=90151622; PubMed=1689240;
Roldan A.L., Cubellis M.V., Masucci M.T.,
Danoe K., Appella E., Blasi F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO0692; NIFH FRXC 2; 1.
PROSITE; PSO0746; NIFH FRXC 1; 1.
Oxidoreductase; Nitrogen fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X07477; CAA3036
PIR; 802219; 802219.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMB;
                                                                                                                                                                                                                                                                                                                                                                                                                                         lomo sapiens (Human)
                    Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content ified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a 8 oxidized ferredoxin + 2 NH(3) + 16 AUF + 16 PROBP
COFACTOR: BINDS ONE 4FE-48 CLUSTER PER DIMER.
SUBUNIT: Homodimer.
SIMILARITY: BELONGS TO THE NIFH / BCHL / CHLL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 m 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.

COFACTOR: BINDS ONE 4FE-4S CLUSTER PER DIMER.
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Primates;
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70.0%;
                                     plasminogen activator.";
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Catarrhini;
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Q9UD69; Q9UEA6; Q9UM92;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altochul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Lichards C., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Schaefer M.J., Ugdin T.B., Toshiyuki S., Casavant T.L., Schaetz T.E., RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H., Ra Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA William M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., AN William M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Fahey J., Helton E., Ketteman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generch A., Schein J.E., Jones S.J.M., Marra M.A., "Generch A., Schein J.E., Jones S.J.M., Marra M.A., "Generch A., Schein J.E., Jones S.J.M., Marra M.A., "Generch A., Schein J.E., Land McGenerch M., Schein J.S., Jones S.J.M., Marra M.A., "Generch M.A., "Generch A., Schein J.S., Jones S.J.M., Marra M.A., "Generch A., Schein J.S., Jones S.J.M., Marra M.A., "Generch M. Schein J.S., Jones M. Schein J.S., Marra M.A., "Generch M. Schein J.S., Marra M.
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"Sequence analysis of a 4.2 Mb region in 19q13.2 between AKT2 and present a survey of the sequence of the sequ
                                                                                                                                                                                                                                                                                    TISSUE=Lung
Zhu F., Jia
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Blasi F.;
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Blood
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"A conserved TATA-less proximal promoter from the urokinase-type plasminogen activ Blood 86:624-635(1995).
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Lamerdin J.E., N
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MEDLINE=93314820; PubMed=8392005;
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"A novel urokinase receptor on
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Lund L.R., Danoe
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                                                                                                                              SEQUENCE OF 1-18 MEDLINE=95329719;
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cloning
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A., De Luca P.,
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21:395-395(1993).
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Genew; HGNC:9053; PLAUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anchored membrane proteins.";
J. Biol. Chem. 268:17539-17546 (1993).
-i- FUNCTION: ACTS AS A RECEPTOR FOR UROKINASE PLASMINOGEN ACTIVATOR.
PLAYS A ROLE IN LOCALIZING AND PROMOTING PLASMIN FORMATION.
MEDIATES THE PROTEOLYSIS-INDEPENDENT SIGNAL TRANSDUCTION
ACTIVATION EFFECTS OF U-PA. IT IS SUBJECT TO NEGATIVE-FEEDBACK
REGULATION BY U-PA WHICH CLEAVES IT INTO AN INACTIVE FORM.
-i- SUBGULIT: Monomer (Probable).
-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(1soform 1). Secreted (isoform 2).
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MEDLINE=90202929; PubMed=2156852;

Behrendt N., Roenne E., Ploug M., Petri T., Loeber D., Ni
Schleuning W.-D., Blasi F., Appella E., Danoe K.;

"The human receptor for urokinase plasminogen activator.

amino acid sequence and glycosylation variants.";

J. Biol. Chem. 265:6453-6460(1990).
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PARTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a
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Hoeyer-Hansen G., Ploug M., Behre
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                                                        L; U08839; AAB60333.1; -.
L; AC005525; AAC32739.1; -.
L; AC006953; AAD17387.1; -.
L; AC006953; AAD17387.1; -.
L; BC002788; AAH02788.1; -.
L; BC925789; AAF1751.1; -.
L; S78532; AAD14289.1; -.
L; A18757; CAA01421.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q03405-3; Sequence-VSP_006714; SIMILARITY: Contains 3 UPAR/Ly6 domains.
DATABASE: NAME=PROW; NOTE=CD guide CD87 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd87.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bvent=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=uPAR1, GPI-anchored;
IsoId=003405-1; Sequence=Displayed;
Name=2; Synonyms=uPAR2, Secreted;
IsoId=003405-2; Sequence=VSP_006715;
Name=3.
                                                                                                                                                                                                          X51675; CAA35981.1; -.

M83246; AAA59862.1; -.

X74039; CAA52191.1; -.

U09346; AAA17979.1; -.

U09347; AAA17978.1; -.

U09937; AAB60690.1; JOIN

U09932; AAB60690.1; JOIN

U09933; AAB60690.1; JOIN

U09933; AAB60690.1; JOIN

U09933; AAB60690.1; JOIN
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S39495; S39495.
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                                                                                                                                                                                                                                                                                                                                                                                            license agreement (S license@isb-sib.ch).
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urokinase-catalyzed
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Hypothetical protein Rv0479c.
RV0479C OR MT0497 OR MTCY20G9.05C.
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GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0015025; F:GPI-anchored membrane-bound
GO; GO:0015025; F:blood coagulation; TAS.
GO; GO:0006935; P:chemotaxia; TAS.
InterPro; IPR001526; LY6 UPAR.
InterPro; IPR001561; U-PAR.
Pfam; PF00021; UPAR LY6; 2.
"Whole genome comparison of laboratory strains."; Submitted (APR-2001) to the
                                                                                   SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen
Fleischmann R.D., Dodson R., G
Peterson J., DeBoy R., Dodson R., G
Kolonay J.F., Nelson W.C., Umayam I
Delcher A., Utterback T., Weidman J
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Bacteria; Actinobacteria; P
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SM00134; LU; 3.
E, PC0000
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393:537-544(1998).
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                                                                                      n J.A., Carpenter L., White O.,
Gwinn M.L., Haft D., Hickey E.,
L.A., Ermolaeva M.D., Salzberg
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RESULT 10
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Best Local
                                                                                                                                                                                                                  729749;
71-APR-1993 (Rel. 25, Lieutur.)
71-APR-1993 (Rel. 25, Last sequence update;
71-APR-1993 (Rel. 39, Last annotation update)
71-APR-1993 (Rel. 39, Last annotation update)
71-APR-1993 (Rel. 39, Last annotation update)
71-APR-1993 (Rel. 25, Lieutur.)

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                                                                                                                                                                                                                or send an email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-HB8 / ATCC 27634;
MEDLINE=92201699; PubMed=1339363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P29749,
01-APR-1993
                    InterPro; IPR002296; N12N6_mtfrase.
InterPro; IPR002052; N6_Mtase.
InterPro; IPR000051; SAM_bind.
PRINTS; PR00507; N12N6MTFRASE.
                                                                                                                                            EMBL; M74795; AAA27488.1;
HSSP; P14385; 2ADM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barany F., Danzitz M., Zebala J., Mayer A.; "Cloning and sequencing of genes encoding t modification enzymes: comparison with the i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculist; Rv0479c; -.
Hypothetical protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                     REBASE; 3523; M.TchHB8I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzymes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus thermophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE TCGA, CAUSES SPECIFIC METHYLATION ON A-4 ON BOTH STRANDS AND PROTECTS THE DNA FROM CLEAVAGE BY THE TTHHBBI ENDONUCLEASE CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-
                                                                                                                                                                                                                                                                                                                                                                                                       adenosyl-L-homocysteine + DNA 6-methylaminopurine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 6; Conserv
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50.0%;
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Pred. No. 30;
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RX MEDLINE-2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G.; Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Capter Y.H.C., Blazej R.G., Champ Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champ M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pietschmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Heiman T.J., Hin J., Liang Y., Lin X.,
RA Mount S.M., My M., Murphy L., Muzny D.M., Nelson D.L.,
RA Menschov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentst K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Polaco D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Willams S.M., Woodage T., Worlber E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinsteck G.M., Weissenbach J.,
RA Willams S.M., Woodage T., Worlby K.C., Wu D., Yang S., Zhao Q., Zhang L.,
Rand D., Yang S., Zhan M., Zhang G., Zhang L.,
Rand D., Yang S., Zhan M., Zhang G., Zhang L.,
Rand D., Yang S., Zhan M., Zhang G., 
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Best Local
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16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Eye imaginal disk;
MEDLINE=93327423; PubMed=7916657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anachronism protein precursor. ANA OR CG8084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibits neuroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 A.J., Garren H., Cheyette B.N.R., Zipursky S.L.;
Drosophila anachronism locus: a glycoprotein secr
bits neuroblast proliferation.";
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RESULT 12
COE1 RAT
ID COE1
AC Q6333
DT 30-MJ
DT 30-MJ
DT 28-FI
DE (TARN
COE1
GN EBF
GN EBF
OC EUAG
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RP SEQ
RX MED
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Best Local S
Matches 6
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30-MAY-2000
30-MAY-2000
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CARBOHYD
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CONFLICT
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CARBOHYD
CARBOHYD
                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transcription factor COE1 (OE-1) (O/E-1) (Ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000).
                                        neurons and their precursors.
-!- SIMILARITY: BELONGS TO THE COE
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE=93309542; PubMed=8321284;
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                (Olfactory neuronal transcription EBF OR EBF1 OR COE1 OR OLF1.
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0011746; ana.
Glycoprotein; Signal; Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003834; AAF58998.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
                                                                    family member.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Expressed exclusively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: NEGATIVELY REGULATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.A., Myers E.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (S an email to license@isb-sib.ch).
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    entry is copyright.
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Rodentia;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38;
Pred. No.
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N-LINKED
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ANACHRONISM PROTEIN.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FE8A43042BB595A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ore 38; DB
red. No. 42;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                (O/E-1) (Early B factor) (Olf-1)
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                                          FAMILY
      It is
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    produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 474;
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                                                                                olfactory receptor
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RESULT
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COE1_HU
Q9UH73,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L24051; AAA41759.1; ALT INIT.
InterPro; IPR001092; HLH basic.
InterPro; IPR002909; IPT TIG.
InterPro; IPR003523; TF COE.
Pfam; PF01833; TIG; 1.
SMART; SM00353; HLH; 1.
SMART; SM00429; IPT; 1.
SMART; SM00429; IPT; 1.
PROSITE; PS01345; COE; 1.
Dranscription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Transcriptional activator which recognizes variations of the palindromic sequence 5'-ATTCCCNNGGGAATT-3' (By similarity).
-!- SUBUNIT: Forms either a homodimer or a heterodimer with a related family member (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE COE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20400007; PubMed=10942392;
Gisler R., Jacobsen S.E., Sigvards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYUH'S;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Transcription factor COEI (OE-I) (O/E-I) (Ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAMOH
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ZN_FING 151 170 C5-TYF
DOMAIN 455 543 SER/TH
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                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
EBF OR EBF1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                   MIM; 164343; -
                                                                                                                 EMBL; AF208502; AAF19643.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blood 96:1457-1464(2000).
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                                                                                            Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                            HGNC:3126;
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5; Conserv
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                                                                                            EBF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         development in r
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InterPro; InterPro;

IPR001092; HLH\_basic. IPR002909; IPT\_TIG. IPR003523; TF\_COE.

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RESULT 14
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; DNA-binding; Nuclear protein; Activator; Developmental protein; Zinc-finger.

NON TER 1 1 1 1 2N FING 146 165 C5-TYPE (POTENTIAL).

DOMAIN 457 545 SER/THR/PRO-RICH.
                                                                                                                                                                                                                                 STRAIN=CD-1; TIBSUSESHING, 9151732;
MEDLINE=97296547; PubMed=9151732;
Wang S.S., Teaf R.Y.L., Reed R.R.;
"The characterization of the Olf-1/EBF-like HLH transcription;"
"The characterization of the Olf-1/EBF-like HLH transcription;"
                                                                                                                                                                                                                                                                                                                                              MEDLINE-93268288; PubMed-8497258;
Travis A., Hagman J., Hwang L., Gross
"Purification of early-B-cell factor
DNA-binding specificity.";
Mol. Cell. Biol. 13:3392-3400(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transcription factor COE1 (OE-1) (O/E-1) (Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q07802;
30-MAY-2000
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SMART; SM00429; IPT; 1.
PROSITE; PS01345; COE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hagman J., Belanger C., Travis A., Turck W., Grosschedl R.; "Cloning and functional characterization of early B-cell factor, regulator of lymphocyte-specific gene expression."; Genes Dev. 7:760-773(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                 development.";
J. Neurosci. 17:4149-4158(1997).
                                                                                                                                                                                                                                                                                                       SUBUNIT, AND ALTERNATIVE SPLICING STRAIN=CD-1; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lymphoid;
MEDLINE=93259462; PubMed=8491377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia, Eutheria,
Name-Short; Synonyms=0;
IBOId=Q07802-2; Sequence=VSP_001112;
TISSUE SPECIFICITY: Expressed at high levels in early B-cells, spleen; lymph node and adipose tissue, and at low levels in heart, brain, skeletal muscle and kidney. In adult expressed in olfactory brain, skeletal muscle and at a lesser extent in Purkinje cells of
                                                                                                                                                                       FUNCTION: Transcriptional activator which recognizes variations the palindromic sequence 5'-ATTCCCNNGGGAATT-3'.
SUBUNIT: Forms either a homodimer or a heterodimer with a relati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR EBF1 OR COE1
                                                                                                                                SUBCELLULAR LOCATION: Nuclear ALTERNATIVE PRODUCTS:
                                                                                     Name=Long; Synonyms=8;
IsoId=Q07802-1; Sequence=Displayed;
                                                                                                                 Event-Alternative splicing; Named isoforms-2
                                                                                                                                                           family member.
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457
586 AA;
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545 S
63845 MW;
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Rodentia;
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Pred. No.
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SER/THR/PRO-RICH.
; D3596C26FEC72CF6 CRC64;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                            Grosschedl R.; actor and characterization of
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                                                                                                                                             (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87-99; 122-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            591
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; Murinae; Mus
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RESULT 15
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Best Local S
Matches 5
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MGD; MGI:95275; Ebf1.

GO; GO:0005515; F:protein binding activity; IPI.

GO; GO:0045941; P:positive regulation of transcript
InterPro; IPR001092; HLH basic.

InterPro; IPR002299; IPF TIG.

InterPro; IPR003523; TF_GOE.

Pfam; PF01833; TIG; 1.

SMART; SM00353; HLH; 1.

SMART; SM00429; IPT; 1.

PROSITE; P501345; COE; 1.
                                                                                                                                                                                                                                 CCAF HUMAN STAN

O60840; O43901;

15-JUL-1999 (Rel. :

15-JUL-1999 (Rel. :

15-SEP-2003 (Rel. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
"An L-type calcium-channel gene mutated in congenital stationary night blindness.";
                                      Strom T.M., Nyakatura G., Apfelstedt-Sylla E., Hellebrand PLOrenz B., Weber B.H.F., Wutz K., Gutwillinger N., Ruether Drescher B., Sauer C., Zrenner E., Meitinger T., Rosenthal
                                                                                                                                                                                                        Voltage-dependent
CACNA1F OR CACNAF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                 MEDLINE=98324776; PubMed=9662399;
                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Developmental
ZN_FING 1
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Developmental protein, Alt
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                            Meindl A.;
                                                                                                 TISSUE=Retina;
                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                            HIS-1364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the cerebellum, heart, kidney, lung, thymus and testis. In embryo expressed in dorsal thalamus and epithalamus, at a lower level in mesencephalon and in the caudal rhombencephalon, in the postmitotic cells of developing retina, highly in developing spinal cord, dorsal root ganglia, trigeminal ganglia and in glossopharyngeal nerve ganglia, in developing inner ear. DEVELOPMENTAL STAGE: First detected at 9.5 dpc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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5; Conserv
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                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                 38, Created)
38, Last sequence update)
42, Last annotation update)
42, calcium channel alpha-1F subunit.
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259
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89
64464 MW;
                                                                                                                          AND VARIANTS CSNB2 ASP-369;
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/FTId=VSP 001112.

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F -> L (IN REF. 1; AP

F -> L (IN REF. 1; AP
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                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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There are no restrictions
ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription,
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               incomplete X-linked
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1 CRC64;
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CHONDLES 45:340-34/(139/).

IN A VARIETY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1F GIVES RISE TO L-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) PHENYLALVILAMINES, BENCOTHIAZEPINES, AND BY OMEGA-AGA-IVA).

PHENYLALVILAMINES, BENCOTHIAZEPINES, AND BY OMEGA-AGA-IVA).

SUBUNIT: VOLTAGE-PEPRINENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPECASES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE SUBUNITS BETA AND DELTA SUBUNITS SUBUNIT IS SUBFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND DELTA SUBUNITS SUBUNIT IS SUBFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY.

FORMING AND VOLTAGE-SENSITIVE SUBUNITS BETA AND DELTA SUBUNITS SUBUNIT IS SUBFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND DELTA SUBUNITS SUBUNIT IS SUBFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY.

SUBCULTURA TO SUBFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY.

FORMING AND VOLTAGE-SENSITIVE SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULARE THE CHANNEL ACTIVITY.

FORMING AND VOLTAGE-SENSITIVE SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULARE THE CHANNEL ACTIVITY.

FORMING AND VOLTAGE-SENSITIVE SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFAR SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFAR SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A SERIES OF POSITIVELY CHARGED AMINO ACTUS AT EVERY THIRD POSITION.

FORMING AND VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACTUS AT EVERY THIRD POSITION.

FOR THE VOLUME AND ACTUS AT EVERY THIRD POSITION.

FOR THE VOLUME AND ACTUS AT EVERY THIRD POSITION.

FOR THE VOLUME AND A
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MIM; 30007
GO; GO:0000
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        InterPro;
InterPro;
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                                                                                                                          InterPro;
InterPro;
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EMBL; AJ224874; CAA12175.1; -.
EMBL; AF235097; -, NOT ANNOTATED CDS.
EMBL; U93305; AAB92359.1; -.
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Meindl A., Rosent
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GO:0005245; I
GO:0006832; I
GO:0007268; I
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                                        :0005891; C:voltage-gated calcium channel complex; TAS.
:0005245; F:voltage-gated calcium channel activity; TAS.
:0006832; P:small molecule transport; TAS.
:0007268; P:synaptic transmission; TAS.
:0007601; P:vision; TAS.
:0007601; P:vision; TAS.
ro; IPR001682; Ca/Na_pore.
ro; IPR0021077; Ca_channel.
ro; IPR002111; Cat_channel_TrpL.
ro; IPR005821; Ion_trans.
ro; IPR005446; LVDCCAlphal.
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IPR005446; LVDCCAlphal.
IPR005820; M+channel_nlg.
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CYTOPLASMIC (POTENTIAL).
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ion; Disease mutation; Vision.
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R -> W (in CSNB2).

/FTId=VAR 001506.

L -> H (in CSNB2).

/FTId=VAR 001507.

E -> V (IN REF. 3).

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hypothetical protein Rv1868 - Mycobacterium tuberculosis (strain H37RV)
(;Species: Mycobacterium tuberculosis
(;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70667
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connocr, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70667
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D70667
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A,Molecule type: mRNA
A,Residues: 1-409 <KIB>
A,Cross-references: EMBL:U45243; NID:g1685090; PIDN:AAC49538.1;
C,Superfamily: laccase
C,Superfamily: laccase
                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-699 <COL> A;Residues: 1-699 <COL> A;Cross-references: GB:Z83859; GB:AL123456; NID:g3261678; PIDN:CAB06119.1; PID:e290717; A;Experimental source: strain H37Rv A;Experimental source: strain H37Rv
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A;Title: Cloning and sequence analysis of laccase-encoding cDNA clones
A;Reference number: JC5229; MUID:97080572; PMID:8921917
A;Accession: T03788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Kiefer-Meyer, M.; Gomord, V.; O'Connell, A.; Halpin, C.; Faye,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: diphenol oxidase; urishiol oxidase
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: T03788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laccase (EC 1.10.3.2) - common tobacco (fragment)
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nes 7; Conserv
                                                                                     Rv1868
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54.4%; Score 43; 40.0%; Pred. No.
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RESULT 5
hypothetical protein DKFZp586E1422.1 - C;Species: Homo sapiens (man) C;Date: 11-Jun-1999 #sequence_revision C;Accession: T08792 R;Koehrer, K.; Beyer, A.; Mewes, H.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Favello, A.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1777 <FAV>
A;Residues: 1-1777 <FAV>
A;Cross-references: EMBL:U41263; PIDN:AAC24428.1; GSPDB:GN00020;
A;Experimental source: strain Bristol N2; clone T19D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T19D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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A;Residues: 1-1257 <SAK>
A;Cross-references: EMBL:AB016532; NID:g3845582; PIDN:BAA34187.1; PID:g3845583
A:Experimental source: strain Sprague-Dawley; brain; clone RG1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Sakamoto, K.; Nagase, T.; Fukui, H.; Horikawa, K.; Okada, T.; Tanaka, H.; Sato, K.; Mi
J. Biol. Chem. 273, 27039-27042, 1998
A;Title: Multitissue circadian expression of rat period homologue (rPer2) mRNA is govern
A;Reference number: Z17833; MUID:98438460; PMID:9765215
                                                                                                                                                                                                                                                                                                                  A; Introns: 36/1; 134/2; 180/1; 622/3; 691/2; 754/1; 1111/2; 1174/1; 1271/3; 1322/2; 168
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A;Accession: T34369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Species: Rattus norvegicus (Norway ra;Date: 20-Sep-1999 #sequence_revision;Accession: T13957
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Pred. No.
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Pred. No. 1.1e+02;
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                   Gassenhuber, J.; Wiemann,
                                                11-Jun-1999 #text_change 13-Aug-1999
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C;Bu, Z.; Goela, D.
Submitted to the EMBL Data Library, December A;Description: The sequence of C. elegans A;Description: The Sequence of C. elegans
                                                                                                                                                                                                           A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-304 <PAR>
                                                                                                                                                                                                                                                              R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1998 A;Reference number: Z20619
A;Accession: T29421
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                                                                                                                                                                                                                                                                                                                                                  C;Species: Streptomyces coelicolor
C;Date: 22-Oct-1999 #sequence_revi
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A; Introns: 139/1; 201/2; 232/1
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A;Experimental source: strain Bristol N2; clone K05F6
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A;Residues: 1-133 <KOE>
A;Cross-references: EMBL:AL050170
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A; Accession: T08792
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SC3A7.03c - Streptomyces coelicolor
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C;Species: Caenorhabditis elegans
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Carbon catabolite repressor MIG1 - yeast (Kluyveromyces marxianus var. lactis)
NAlternate names: finger protein MIG1
C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Oct-1999
C;Accession: S66480
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R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Nature 402, 769-777, 1999
                                                          A;Title: The MIG1 repressor from Kluyveromyces lactis: cloning, sequencing A;Reference number: $66480; MUID:95402208; PMID:7672126 A;Accession: $66480
                                                                                                                     R;Cassart, J.P.; Georis, I.; Oestling, J.; Ronne, H.; Vandenhaute, FEBS Lett. 371, 191-194, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Bevan, M.; Brandt, P.; Dose, S.; submitted to the Protein Sequence!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F16A16.200 - Arabidopsis thaliana (fragment)
C;Bpecies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C;Accession: T04530
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                                                                                                                                                                                                                                                               S66480
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A;Experimental source: cultivar Co
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A; Accession: T04530
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C/Species: Arabidopsis thaliana (mouse-ear cress)
                    A, Molecule type: DNA
A;Residues: 1-474 <CAS>
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Database, February
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Gene 178, 205-207, 1996
A;Title: Cloning and sequence analysis of laccase-encoding cDNA clones
A;Reference number: JC5229; MUID:97080572; PMID:8921917
                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule transparent transparen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: strain CBS A;Note: the source is designated C;Genetics:
                                                                                                                     A; Mobile element: transposon Tn5053 C; Superfamily: Klebsiella transposase
                                                                                                                                                                                                                                                                                                                                                            A;Title: Tn5053, a mercury resistance transposon with integron's ends A;Reference number: S32795; MUID:93253772; PMID:8387603 A;Accession: S32799
                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kholodii, G.Y.; Yurieva, O.V.; Lomovskaya, O.L.; Gorlenko, J. Mol. Biol. 230, 1103-1107, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein 1 - Xanthomonas sp. transposon Tn5053 (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S32799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: JC5229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: p-diphenol:02 oxidoreductase; urushiol oxidase C;Species: Nicotiana tabacum (common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: DNA binding; transcription F; 28-78/Region: zinc finger CCHH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: MIG1
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                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: S32799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Xanthomonas sp. .
;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 11-Jan-2000
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Similarity 6; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.; Gomord, V.; O'Connell, A.; Halpin, C.; Faye,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                            49.4%;
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                            Score 39;
Pred. No.
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Pred. No.
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Pred. No. 79;
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as Kluyveromyces lactis
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                            46;
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                                                        <u>د.</u>
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                                                        Length 203;
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                                                                                                                                                                                                             December 1992
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Mismatches

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Gaps

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L.; Hyman, R.W.; Jones, T.; Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation
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E95889
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Development 114, 417-433, 1992
A;Title: Hair follicle differentiation: expression, structure
A;Teference number: I46409; MUID:92274852; PMID:1375545
A;Accession: I46409
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                              A;Cross-references: GB:AL591985; PIDN:CAC48781.1; PID:g15140254; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                    R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: E95889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable dehydrogenase protein [imported] - Sinorhizobium meliloti (strain 1021)
C; Species: Sinorhizobium meliloti
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A;Residues: 142-190,192-251 <CRE>
A;Note: 51-Lys and 52-Lys were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Amino acid sequences of alpha-helical segments A;Reference number: A02954; MUID:79020757; PMID:581264 A;Accession: A02954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Crewther, W.G.; Inglis, A.S.; McKern, Biochem. J. 173, 365-371, 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Nov-1984 #sequence_revision 15-May-1998 #text_change 10-
C;Accession: 146409; A02954; S22025
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N;Alternate names: intermediate filament protein KII-9; low-sulfur keratin
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F;126-253/Region: coil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns:
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                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-749 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: cytoskeletal keratin; hair; intermediate filament; keywords; coiled coil; cytoskeleton; hair; intermediate filament;
                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
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led coil 1 #status predicted
led coil 2 #status predicted
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                                                                                                           D.H.; Kiss, E.; Komp, C.; Lelaure
S.; Wells, D.H.; Wong, K.; Yeh, K
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RESULT 15
JC2129
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A;Residues: 1-190, 'D', 192-942 < PAL>
A;Residues: 1-190, 'D', 192-948, 'NID:g914097; PIDN:AAB33345.1; PID:g9
A;Cross-references: EMBL:875546; NID:g914097; PIDN:AAB33345.1; PID:g9
A;Experimental source: fetal brain
R;Palmer, R.H.; Ridden, J.; Parker, P.J.
FEBS Lett. 356, 5-8, 1994
A;Title: Identification of multiple, novel, protein kinase C-related
A;Reference number: $51020; MUID:95080426; PMID:7988719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: JC2129
A;Molecule type: mRNA
A;Residues: 1-942 <MUK>
A;Cross-references: GB:D26181; NID:g473712; PIDN:BAA05169.1;
A;Cross-references: GB:D26181; NID:g473712; PIDN:BAA05169.1;
A;Palmer, R.H.; Ridden, J.; Parker, P.J.
Bur. J. Blochem. 227, 344-351, 1995
Bur. J. Blochem. 227, 344-351, 1995
A;Title: Cloning and expression patterns of two members of a A;Reference number: I53327; MUID:95154310; PMID:7851406
A;Accession: S67526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: protein-kinase-C-related kinase PRK1 C;Species: Homo sapiens (man) C;Date: 30-Sep:193 #sequence revision 20-Aug-1994 #text_change C;Accession: JC2129; S67526; S51020; I53327 R;Mukal, H; Ono, Y.
                                                                                                                                                                                                   C;Comment: This protein has a protein kinase domain related to prote;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases;C;Keywords: ATP; leucine zipper; phosphotransferase; protein kinase;39-66/Region: basic zipper motif F;70-287/Region: leucine zipper motif F;70-87/Region: protein kinase homology <KIN> F;621-629/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 700-799, 'A' <PA2>
                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S51020
A;Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 199, 897-904, 1994
A;Title: A novel protein kinase with leucine zipper-like
A;Reference number: JC2129; MUID:94183274; PMID:8135837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase PKN
N;Alternate page
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RESULT 1
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  Q8VE51 PRELIMINARY; PRT; 336 AA.

Q8VE51;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to D123 gene product (Hypothetical protein)
sequence AA959893) (D123 homolog).

AA9598933.
                                       the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                               SEQUENCE FROM N.A. MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                          Strausberg R.;
Submitted (FEB-2002)
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Submitted (DEC-2001)
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EMBL; BC019753; AAH19753.1;
EMBL; BC022972; AAH22972.1;
EMBL; BC024787; AAH24787.1;
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TISSUE=Eye;
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023821; AAH23821.1; -.
SEQUENCE 336 AA; 38804 MW; 1E48B616B2567A76 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Okuda A., Kimura G
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Mammalia; Eutheria;
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Mammalia, Eutheria,
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"An amino acid change in novel protein D123 is responsible temperature-sensitive G1-phase arrest in a mutant of rat fi
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                                                                                                                                                           336 AA;
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
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                                                                                                                                                        38812 MW;
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80.0%;
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Last annotation update)
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                                                                                      Score 47;
Pred. No.
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Pred. No.
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Pred. No.
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Sciurognathi;
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                                                                                                                                                           6E1D1379A2612934 CRC64;
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                                                                 Mismatches
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                                                                                                         DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
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P93368
ID P933
AC P93
                       DRRETT A A RREP DER RETT A COCCE
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                  Pfam;
Pfam;
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Query Match
Best Local S
Matches 7
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Q8S5R3,
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
Putative copia-type pol p
0J1136B01.16,
Oryza sativa (Rice).
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NON_TER 1
SEQUENCE 409 A
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P93368;
01-MAY-1997
01-MAY-1997
01-MAR-2003;
                                                                                                                 STRAIN=Nipponbare;
McCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirk
McCombie W.R., de la Bastide M., Spiegel L., Bell M., Bakk
Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Bakk
Santos L., Miller B., Katzenberger F., Muller S., King L., Y.
O'Shaughnessy A., Palmer L., Dedhia N.,
"Genomic sequence for Oryza sativa, Nipponbare strain, clone
OJ1136801, from Chromosome 10, complete sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                     EMBL; AC108883; AAM08642.1;
Gramene; Q8S5R3; -.
InterPro; IPR001584; Rve.
InterPro; IPR001878; Znf_CCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 178:205-207(1996).
EMBL; U45243; AAC49538.1; -.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97080572; PubMed=8921917;
Kiefer-Meyer M.C., Gomord V., O'Connell A., Halpin
"Cloning and sequence analysis of laccase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
01-MAR-2003 (TrEMBLrel. 23,
Diphenol oxidase (EC 1.10.3)
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4530;
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PF00665; rve; 1.
PF00098; zf~CCHC; 1.
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63.6%;
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                                   znf_cchc
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21, Last sequence 22, Last annot polyprotein.
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Last annotation update)
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.2) (Fragment).
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Pred. No.
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A clones from
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Best Local S
Matches 9
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Q8GS39;
01-MAR-2003
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01-MAR-2002
01-OCT-2002
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SEQUENCE FROM N.A.

STRAIN-CV. Nipponbare;

Wato H., Suroh K., Minamikawa T.;

Widentification, cDNA Cloning and Possible Roles of Seed Asparaginyl Endopeptidase, REP-2.";

Submitted (MAR-2002) to the RBBL/GenBank/DDBJ databases.

EMBL; AB081464; BAC41386.1; -.

EMBL; AB081465; BAC41387.1; -.
                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
Eukarycta; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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Eukaryota; Viridiplantae; Etreptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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PROSITE; PS50158; ZF CCHC; 1.
Polyprotein.
SEQUENCE 1866 AA; 212916 M
                                                                                                                                                                                                                                                                                                                Asparaginyl REP2.
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Bi X.-Z., Khush G.
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(TrEMBLrel. 23, Last sequence update)
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endopeptidase REP-2.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                           Embryophyta; Tracheophyta;
a; Poales; Poaceae;
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RESULT 8
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ID Q8QF
AC Q8QF
AC Q8QF
DT 01-J
DT 01-J
DT 01-M
DE EBF1
OS Raja
OC Euka
OC Elas
OC Elas
OC Raji
INT
CAN
DT 11
OX NCB1

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P95147
ID P951
              AC CONTRACTOR OF THE PROPERTY 
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Best Local S
Matches
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EMBL; AY079197; AAL86576.1; -.
InterPro; IPR001092; HLH_basic.
InterPro; IPR002909; IPT_TIG.
InterPro; IPR003503; TF_COE.
Pfam; PF01833; TIG; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P95147; PRELIMINARY;
P95147; P15147;
01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
01-OCT-2002 (TrEMBLrel. 22,
MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein Rv1868.
RV1868 OR MTCY359.05C OR MT1917.
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                                                                                                                                                                                                                                                   STRAIN=H37Rv;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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SMART; SM00429; IPT; 1.
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Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002
01-JUN-2002
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NCBI_TaxID=33514;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson M.K., Miracle A.L.,
Litman G.W., Rothenberg E.V.
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Pred. No.
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01-OCT-2000
01-OCT-2000
01-MAR-2003
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Q8BIF4;
01-MAR-2003
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Nature 393:537-544(1998).
Hypothetical
                                                                                                                                                                                                                     the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome | 0,710 full-length cDNAs."; 60 full-length cDNAs."; 84 Nature 420:563-573(2002).

EMBL; AK078480; BAC37299.1; -. SEQUENCE 504 AA; 53792 MW; EFE33F
                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to similar to calcineurin binding protein 1
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White Of Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Miku
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[2]
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-E235L/6J; TISSUE-Mullerian
MEDLINE-2235L/63; PubMed=12466851;
The FANTOM Consortium,
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Hypothetical protein; Complete SEQUENCE 699 AA; 74396 MW;
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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TIGR; MT1917;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
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Last annotation update)
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Pred. No.
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Sciurognathi;
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RESULT 12
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Q9Z301;
01-MAY-1999
                                                                                                                                                                                    nucieus in the brain.";
J. Biol. Chem. 273:7039-27042(1998).
EMBL; AB016532; BA334187 1; -.
InterPro; IPR001610; PAC.
InterPro; IPR001014; PAS domain.
SMART; SM00086; PAC; 1.
SMART; SM00081; PAS; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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WormPep; H43E16.1; CE19949.
Hypothetical protein.
SEQUENCE 1203 AA; 120104
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Submitted (MAR-2000)
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"The seguence of C. e
Submitted (MAR-1999)
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STRAIN=Bristol N2;
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Best Local
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TISSUE=Uterus;

Kochrer K., Beyer A., Mewes H

Submitted (MAR-1999) to the E

EMBL; ALOS0170; CAB43306.1; -

Hypothetical protein.

NON TER 1
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01-OCT-2001 (TrEMBLrel. 18, Lae
01-MAR-2003 (TrEMBLrel. 23, Lae
Hypothetical 187.1 kDa protein.
T19D12.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Y3Y1 PRELIMINARY; PRT; 133 AA.
Q9Y3Y1,
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
DKFZP586E1422.
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Q22579;
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; U41263; AAC24428.2; -. Wormbep; T19D12.1; CE28677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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1844 AA; 187133 MW;
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Primates;
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EMBL/GenBank/DDBJ
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Last annotation update)
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Pred. No.
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databases.
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01-JUN-1998 (TrEMBLrel. 06, Las
01-MAR-2003 (TrEMBLrel. 23, Lass
Hypothetical 31.6 kDa protein.
K05F6.10.
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Hypothetical
SEQUENCE 27
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044870;
                                                                                                                                                           "Direct Submission.";
Submitted (AUG-2001) to the
                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.", Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613;
                                                                                                                                        EMBL; AF040653; AAB95023.1; WormPep; K05F6.10; CE17168.
                                                                                                                                                                                                                                Du Z., Goela D.; "The sequence of C.
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Rhabditidae; Peloderinae;
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nilarity 57.1%;
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277 AA; 3
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N2;
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cinae; Caenorhabditis.
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63.6%;
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EMBL/GenBank/DDBJ
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                                                                                        Score 41; DB
Pred. No. 23;
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Pred. No. 11;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

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Sequence 9, Appl
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Publication No.
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TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
TITLE OF INVENTION: DOMAIN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION FILE REFERENCE: 65823/JPW/PT
                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/230,111C CURRENT FILING DATE: 1999-05-17
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SOFTWARE: Patentin Ver.
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APPLICANT: Yanaç
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                                                                                                            OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:source:synthesized
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DATE: 1997-08-18
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                                               DATE: 1997-08-18
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Query Match
Best Local Similarity
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Thes 9; Conserv
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US-09-954-737-9
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                                                                                                                         Sequence 9, Application US/09954737
Patent No. US20020110860A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/244,782
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 178
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APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2001-11-01
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
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PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
                                          APPLICANT:
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PPLICANT: Jongbloed, Jan D.H.
PPLICANT: Mueller, Joorg P.
PPLICANT: Van Dijl, Jan M.
ITLE OF INVENTION: Twin-Arginine Translocation in
ILE REFERENCE: GC634-2
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Pred. No.
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DATE: 1997-09-12
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US-09-741-669-421
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-954-737-9
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APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essent

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITEA, 011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21
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SEQ ID NO 421
LENGTH: 346
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Best Local Similarity
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                                                                                                                                                                                 APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US 60/233,610
PRIOR FILING DATE: 2000-09-18
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Pred. No.
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Pred. No. 3.4e+02;
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                                                                                                         RESULT 10
US-09-766-511B-26
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US-09-815-242-10206
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PRIOR APPLICATION UNMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION UNMBER: 60/257,931
PRIOR APPLICATION UNMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION UNMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                    GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10206
LENGTH: 346
                                                                       Sequence 26, Application US/09766511B Publication No. US20030170621A1
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9362
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
APPLICANT: MCCARTHY, Sean A
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
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HORIKAWA, HIROSHI
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Pred. No. 4.6e
3; Mismatches
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Pred. No.
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RESULT 11
US-10-188-495-51
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                                                                              ; ORGANISM: Homo sapiens
US-10-188-495-51
                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 51
LENGTH: 498
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SEQ ID NO 26
LENCTH: 498
TYPE: PRT
              Query Match
Best Local
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Best Local (
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: POLYPEPTIDES HAVING DIAGNOSTIC,
FILE REFERENCE: 10147-11U2
CURRENT APPLICATION NUMBER: US/10/188,495
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR PILING DATE: 2000-06-16
PRIOR PILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR PILING DATE: 1999-06-29
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APPLICANT:
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PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/345,680
PRIOR FILING DATE: 1999-06-30
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NUMBER OF SEQ ID NOS: 100
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PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
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PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC, PREV
TITLE OF INVENTION: THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-65
                                                                                                                     TYPE: PRT
Local Similarity 66.
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81 FLFLNNNFI 89
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KIRST, Susan J
MYERS, Paul S
                                                                                                                                                                                                                                                                                                                                                                                                HOLTZMAN, Douglas A. FRASER, Christopher C. SHARP, John D.
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                50.7%;
Score 36; DB 12; Length 498; Pred. No. 4.9e+02; Mismatches 0; Indels
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Pred. No. 4.9e+02;
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RESULT 14
US-09-764-898-163
) Sequence 163, Application US/09764898
) Patent No. US20020090673A1
. GENERAL INFORMATION:
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US-09-764-898-183
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SEQ ID NO 51
LENGTH: 498
TYPE: PRT
ORGANISM: Homo sapiens
US-10-189-123-51
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SEQ ID NO 183
LENGTH: 552
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PUZO1
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                               Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                                                                                                                                                                 Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 311
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CURRENT FILING DATE: 2002-07-02
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APPLICANT: FRASER, Christopher C.
APPLICANT: SHARP, John D.
APPLICANT: BARNES, Thomas S.
APPLICANT: BARNES, Thomas S.
APPLICANT: BARNES, THOMAS S.
BITTE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC,
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Pred. No. 5.5e+02;
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Pred. No.
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4.9e+02;
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; NAME/KEY: SITE
; LOCATION: (393)
; OTHER INFORMATION: Xaa equals any of the naturally occurring
US-09-764-898-163
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LENGTH: 553
TYPE: PRT
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Matches
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      Matches
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APPLICANT:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ01
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-06-30
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PRIOR APPLICATION NUMBER: US 09/345,680
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PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 09/342,364
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CURRENT APPLICATION NUMBER: US/09/766,511B
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HOLTZMAN, Douglas A
APPLICANT: KHODADOUST, Mehran M
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC,
TITLE OF INVENTION: THERAPEUTIC, AND OTHER USES
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PRIOR FILING DATE: 1999-06-14
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                                                                                                 ORGANISM: Homo
                                                                                                                         TYPE:
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                                                                                                                                        LENGTH: 591
      Local Similarity 66.
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les 8; Conser
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SHARP, John D
BARNES, Thomas S
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MYERS, Paul S
WRIGHTON, Nicholas
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                    50.7%;
66.7%;
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    Score 36; DB
Pred. No. 5.9e
3; Mismatches
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Pred. No.
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Mismatches 3
0.9e+02;
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PRE

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Db 81 FLFLNNNFI 89

Search completed: November 26, 2003, 12:38:40
Job time: 28.1084 secs

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Minimum DB
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 2000000000
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1: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

5: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

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7: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1107863 seqs, 158726573 residues
                                                               | SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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40	41	42	42	42	45	45	45	71	Score
56.3	57.7	59.2	59.2	59.2	63.4	63.4	63.4	100.0	Query Match
183	465	106	106	60	725	682	682	15	Length
22	22	20	20	23	21	23	21	19	8
AAU19348	ABG03158	AAY55733	AAY55732	ABP03996	AAG38851	ABB92235	AAG25645	AAW50174	DB ID
Human G protein-co	Novel human diagno	FKHL6 forkhead dom	FKHL5 forkhead dom	Human ORFX protein	Arabidopsis thalia	Herbicidally activ	Arabidopsis thalia	Signal-transducing	Description

Inhibition of signal transduction - by inhibiting binding between a signal-transducing protein and a cytoplasmic protein, for treating

WPI; 1998-145347/13.

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RESULT 1
AAW50174
ID AAW5
XX
AC AAW5
XX
PRINCESSES
                                                                                                                                                               Inhibition, specific binding, signal-transducing protein, cytoplasmic protein; proliferation; cancer cell; apoptosis, virally infected cell.
                                        Sato T,
                                                                           22-JUL-1996;
                                                                                                                                               Synthetic.
                                                                                                                                                                                                   Signal-transducing protein carboxy-terminal peptide
                                                                                                                                                                                                                                       AAW50174;
                                                                                                                                                                                                                                                        AAW50174 standard; peptide; 15
                                                                                             18-JUL-1997;
                                                                                                             12-FEB-1998.
                                                                                                                               WO9805347-A1.
                                                                                                                                                                                                                     16-JUL-1998 (first entry)
                                                          (UYCO ) UNIV COLUMBIA NEW YORK.
                                        Yanagisawa J;
                                                                           96US-0681219.
                                                                                             97WO-US12677.
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FXRXCCCCCCCXXX
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Best Local S
Matches 15
25-FEB-1999

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09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-MAY-1999

06-MAY-1999

07-MAY-1999

07-MAY-1999

11-MAY-1999

11-MAY-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel composition is capable of inhibiting specific binding between a signal-transducing protein (STP) having the carboxy-terminal sequence (Ser/Thr)-Xaa-(Val/IIe/Leu), where Xaa = any amino acid (e.g. the present peptide), and a cytoplasmic protein (CP) containing the sequence AAW50162 or AAW50163. The composition can be used to inhibit the proliferation of cancer or virally infected cells, or induce apoptosis in cancer or virally infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG25645 standard; Protein; 682 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA;
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                 99US-0121825

99US-0125588

99US-0125788

99US-0126785

99US-0127462

99US-0128214

99US-0129845

99US-0130449

99US-0130491

99US-0130491

99US-0131491

99US-0132486

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99US-0134221
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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4.4e-06;
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27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
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19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
21-MAY-1999;
 99US-013840.
99US-0139119.
99US-0139452.
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99US-0139456.
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S-0137222.
S-0137528.
S-0137502.
S-0137724.
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S-0135629.
S-0136021.
S-0136392.
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RESULT 3
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Best Local S
Matches 9
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26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016) for harbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                   Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                           Sequence
                                                                                                                                                                                                                                                         organisms
                                                                                                                                                                                                                                                                                                                                         Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB92235
                                                                                                                  useful as herbicides.
                                                                                                                                                                                                                                   Claim 5; SEQ ID NO 1446; 261pp +
                                                                                                                                                                                                                                                                                                                   WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2001; 2001WO-EP09892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2002
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9; Conserv
                                              Similarity
9; Conserv
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                     LASEFLFLSNSFL 15
 LASSFLWIGNSFL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 682
                                           63.4%;
nilarity 69.2%;
Conservative
                                                                                           682
                                                                                                                                                                                                                                                                                                                                         Weidler M;
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99US-0161360.
99US-0161361.
99US-0161920.
99US-0161923.
99US-0161993.
99US-0162142.
                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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69.2%;
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                                             Score 45; DB Pred. No. 12; 2; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1446.
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                                                                  Length 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 682;
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                                              Indels
                                                                                                                                                                                                                                                                                 acid sequences
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                                              Gaps
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27-JUL-1999
02-AUG-1999
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9908-0145919.
9908-0146386.
9908-0146386.
9908-0146386.
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(first entry)  thaliana protein; 725 AA.  thaliana protein fragment SEQ ID NO: 479  thification; signal transduction pathway; on assay; genetic mapping; gene expressio sequence.  thaliana.  2.  2000EP-0301439.  99US-0121825.  99US-0125788.  99US-0125788.  99US-0126785.  99US-0126785.  99US-0132484.  99US-0132484.  99US-0132486.  99US-0132486.  99US-0132486.  99US-0132486.  99US-0132486.  99US-0134218.  99US-0134218.  99US-0134286.  99US-	(Eirst entry)  (Eirst entry)  (Eirst entry)  (Eirst entry)  (Exhilana protein fragment SEQ ID NO: 47990.  (Eirst entry)  (Eirst entry)  (Exhilana protein fragment SEQ ID NO: 47990.  (Exhilana protein fragment SEQ ID NO: 47990.  (Exhilana)  (Eirst entry)  (Ethaliana protein fragment SEQ ID NO: 47990.  (Eirst entry)  (Eirst entry)  (Eirst entry)  (Eirst entry)  (Eirst entry)  (Ethaliana protein fragment SEQ ID NO: 47990.  (Ethaliana)  (Eirst entry)  (Ethaliana protein fragment SEQ ID NO: 47990.  (Ethaliana)  (Ethaliana protein fragment SEQ ID NO: 47990.  (Ethaliana)  (Ethaliana protein fragment SEQ ID NO: 47990.  (Ethaliana protein fragment SEQ ID NO: 47990.  (Ethaliana)  (Ethaliana)	4-JUN 6-JUN 6-JUN 7-JUN 8-JUN 8-JUN 8-JUN	- MAY - MAY - MAY - MAY - MOU - JUN - MAY - MAY	0-APR- 4-MAY- 5-MAY- 6-MAY- 7-MAY- 1-MAY- 4-MAY- 4-MAY- 4-MAY- 4-MAY- 4-MAY- 9-MAY- 9-MAY-	05 MAR-199 05 MAR-199 23 MAR-199 25 MAR-199 25 MAR-199 29 MAR-199 06 APR-199 08 APR-199 16 APR-199 11 APR-199 21 APR-199 21 APR-199 23 APR-199 28 APR-199 28 APR-199		RESULT 4 AAG38851 ID AAG38851 st XX AAG38851; XX AAG38851; XX 18-OCT-2000 XX Arabidopsis XX XX XX Protein ide KW Protein ide KW hybridisati
0 1	pathway; promoter;			** ** ** ** ** ** ** ** ** ** ** ** **		sequence. thaliana. 2. 2. 2000EP-0301439.	andard; Protein; 725 AA.  (first entry)  thaliana protein fragment SEQ ID NO: 479  thication; signal transduction pathway; on assav: genetic mapping; gene expressio
18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 21-JUN-1999 22-JUN-1999 23-JUN-1999 23-JUN-1999 23-JUN-1999 13-JUN-1999 14-JUN-1999 16-JUN-1999 16-JUN-1999 17-JUN-1999 18-JUN-1999 18-JUN		9US-0148 9US-0148 9US-0148 9US-0149 9US-0149 9US-0149 9US-0149	9US-014 9US-014 9US-014 9US-014 9US-014 9US-014 9US-014 9US-014 9US-014	9003-0145 9003-0145 9003-0145 9003-0145 9003-0145 9003-0145 9003-0145 9003-0145 9003-0145 9003-0145	99US-0144 99US-0144 99US-0144 99US-0144 99US-0144 99US-0144 99US-0144 99US-0144 99US-0144 99US-0144 99US-0144	9US-014 9US-014 9US-014 9US-014 9US-014 9US-014 9US-014 9US-014	9US-013 9US-013 9US-013 9US-013 9US-013 9US-013 9US-013 9US-013 9US-013

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27-AUG-1999;
24-JUN-2002
               ABP03996;
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                                                                                                        Similarity 69.: 9; Conservative
                                                                        LASSFLWIGNSFL 82
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(first entry)
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                               Protein;
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                                                                                                                                                       The present invention describes substantially purified human proteins CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a gyadrome associated with ORFX associated disorder. ORFX polyuncleotide sequences can be used in gene therapy. ORFX sequences can be used in the CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver, CC psoriasis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, disorders related to organ (ransplantation, cardiovascular diseases, disorders mellitus, systemic (cupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders infectious (diseases, autoimmune tipscriditis, myasthenia gravis, graft-versus-host CC diseases and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, conservation injury in various tissues and conditions resulting from the perfection or regeneration and treatment of lung or liver fibrosis.

CC reperfusion injury in various tissues and conditions resulting from the perfection of the printed disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                       Sequence
                                                                                                                                                                                       N.B. The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABN19748.
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29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID 7974; 1037pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-2001; 2001WO-US10836.
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                                                                         Similarity 50.7; Conservative
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                                                                                                                                                             Forkhead transcription factor gene; transgenic animal; drug screening.
                                                                                                                                                                                                                                    FKHL6 forkhead domain fragment.
                                                                                                                                                                                                                                                                                                                                AAY55733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methodology. The products can be used for diagnosis, prognosis, monitoring, prevention and treatment of glaucoma. They can also be used for the production of transgenic animals and drug screening. Sequences AAY55722-739 represent forkhead domains of different members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a human forkhead transcription factor gene, FKHL7. The FKHL7 protein can be produced by standard recombinant methodology. The products can be used for diagnosis, prognosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human forkhead transcription factor e.g. develop products for the diagnosis -
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                        21-OCT-1999.
                                                                      WO9953060-A2
                                                                                                               Unidentified
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22-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                            standard;
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98US-0083352.
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RESULT 8
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N-PSDB;
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                              diagnostics, forensics, responsible for genetic biodiversity -
                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #3149
                                                                                                                                                                                                                                                                                                                                                                                            ABG03158 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human forkhead transcription e.g. develop products for the diagnosis -
                                                                                                                                                                  31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                       11-OCT-2001.
                                                                                                                                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                      ABG03158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY55722-739 represent forkhead domains of different memhers FKHL-family of genee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-620429/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1998;
22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-1999;
                                                                                                                     Drmanac RT,
                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sheffield VC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IOWA ) UNIV
                                                                                      2001-639362/73
DB; AAS67345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IDLASEFLFLSNSF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDPASEFMFENGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                    Liu C,
                                                                                                                                                                 2000US-0540217.
2000US-0649167.
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98US-0083352
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                                                                                                                                                                                                                                                                                                                                                                                             Protein; 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.2%;
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Pred. No.
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Claim

20;

SEQ ID

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33517; 103pp; English

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RESULT 9
AAU19348
ID AAU1
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CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC of the sequence data for this patent did not appear in the printed content of the printed of the formal directly from WIPO are formal directly from WIPO are formal directly from WIPO are formal directly from WIPO.
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Best Local S
Matches
                                                        08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; G protein-coupled receptor; nGPCR-x; antiviral; analgesic; cytostatic; cardiant; antidiabetic; anoretic; hypotensive; hypertensive; antiparkinsonian; nostropic; neuroprotective; antidepressant; viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain; cancer; metabolic disease; cardiovascular disease; type 2 diabetes; obesity; anorexia, hypotension, hypertension; myocardial infarction; atherosclerosis; harkinson's disease; psychosis; neurological disorder; schizophrenia; migraine; major depression; anxiety; mental disorder; manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                               WO200166751-A2
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                               08-MAR-2001; 2001WO-US07370
                                                                                                                                                                                                                                                                                                       13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human G protein-coupled receptor nGPCR-2274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU19348 standard; Protein; 183 AA.
(PHAA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
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9, Conserv
  PHARMACIA & UPJOHN CO
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                                                           2000US-0187584.

2000US-0187637.

2000US-0187639.

2000US-0187707.

2000US-0187707.

2000US-0187709.

2000US-0187709.

2000US-0187709.
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                                                                                                                                                                                                                     2000US-0187583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                        2000US-0188290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $
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Pred. No.
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43;
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptors termed nGPCR-x nGPCR-x polynucleotides, polypsytides, and modulators may be used in the treatment of diseases and conditions such as infections, such as viral infections caused by HIV-1 (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, annoraxia, hypotension, hypertension, myocardial infarction, atherosclerosis), Parkinson's disease, and psychotic and neurological disorders, including schizophrenia, migraine, major depression, anxiety, mental disorder, manic depression, and dyskinesias, such as Huntington's disease or Tourette's Syndrome and many other diseases and syndromes listed in the specification. modulators, may also be used in diagnostic assays for such diseases or conditions. The present sequence represents a G protein-coupled receptor
                                                                                                    27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                                                                                               group A streptococcus; Strept antiinflammatory; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         termed nGPCR-x, useful in the treatment a infections, cancers and mental disorders schizophrenia) -
               Telford J,
Tettelin H;
                                                                                                                                                                                                                                                   Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                             Streptococcus; GAS; GBS;
                                                                                                                                                                                                                                                                                                                                         Streptococcus polypeptide SEQ ID NO 9242
                                                                                                                                                                                                                                                                                                                                                                        02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding G protein-coupled receptors termed nGPCR-x, useful in the treatment and diagnosis of viral
                                                                                                                                                              29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                           02-MAY-2002
                                                                                                                                                                                                                         WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                       ABP30033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel isolated nucleic acid molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-536779/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Page 250-251; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
                                                        CHIRON SPA.
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLFLSNSF
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                           Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.3%; Score 40; DB llarity 100.0%; Pred. No. 24 Conservative 0; Mismatches
                                                          GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,
                                                                                                                                                                                                                                                                               S; group B streptococcus; Streptococcus agalactiae;
Streptococcus pyogenes; antibacterial;
ction; vaccine; meningitis; gene therapy.
                             Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                 ₿
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                             Grandi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 183;
                             ຸດ
                             Fraser C;
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RESULT 11
AAU14133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                   WPI; 200
N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-352536/38
N-PSDB; ABN70664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antingal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                               WO200155437-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human novel protein
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                                                                                                                                                                                    25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                                  25-JAN-2001; 2001WO-US02623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombolytic;
Parkinson's d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU14133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus proteins.
                                                                                                                                      (HYSE-) HYSEQ INC
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                                                                                       ΥT,
                                                                                                                                                                                                                                                                                                                                                                             sapiens.
                                           2001-451939/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                           regeneration; immune
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                     AAS22438
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                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280
                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogen; antibody; gene therapy; neurological isease; inflammatory disorder; cancer; asthma; or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              relates to a protein (ABP25413-ABP30895)
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                                                                                          Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                           disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder;
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RESULT 12
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ID AAM90853
AC AAM90
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Best Local (
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                          04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immu cytostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and i The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen SEQ ID NO:18446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM90853 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                       31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               дам90853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388
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2000US-0189874.

2000US-0190076.

2000US-0198123.

2000US-0205515.

2000US-0209467.

2000US-0214886.
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                                                                                                                                                                                          2000US-0184664
2000US-0186350
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75.0%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune/haematopoietic
ine; metastasis.
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No.
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78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and infection.
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0-JUN-2000; 7-JUL-2000; 7-JUL-2000;

2000US-0215135. 2000US-0216647. 2000US-0216880. 2000US-0217487. 2000US-0217496. 2000US-0218290. 2000US-0220963.

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Nucleic acids useful for premetastasis -
                                                                                                                                                  WPI; 200
N-PSDB;
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20-OCT-2000
20-OCT-2000
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08-NOV-2000
017-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                               Claim
                                                                                                                                                                                                           (HUMA-)
                                                                                                                                                  2001-483426/52.
DB; AAK63634.
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                                                                                                                                                                                                            HUMAN
                                                                                                     cids encoding 
r preventing, (
                                                                               SEQ ID
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2000US-0241808

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2000US-0246478

2000US-0246523

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2000US-0246528

2000US-0246511

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2000US-0251868

2000US-0251868

2000US-0251899

2000US-0251899

2000US-0251899
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                                                                                                                                                                                    SC,
                                                                              18446; 3071pp +
                                                                                                                                                                                                            SCI
                                                                                                               human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                     Ruben
                                                                                                                                                                                                            INC
                                                                                                                                                                                     SM;
                                                                               Sequence Listing;
                                                                                                                 antigen
                                                                               English.
                                                                                                                   polypeptides, and
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2000US-022547 2000US-0225214 2000US-022527 2000US-022527 2000US-022527 2000US-022547 2000US-022548 2000US-022548 2000US-022548 2000US-02258 2000US-02298 2000US-022944 2000US-022945 2000US-023945 2000US-023943 2000US-0231244 2000US-0233249 2000US-0233498 2000US-0235836

14-AUG-2000
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14-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
01-SEP-2000
02-OCT-2000
02-OCT-2000
02-OCT-2000
02-OCT-2000

2000US-0236367 2000US-0233688 2000US-0236369 2000US-0236370 2000US-0237037 2000US-0237037 2000US-0237039 2000US-0237039 2000US-0237039 2000US-023935 2000US-023937 2000US-0241786

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RESULT 13
ABU00902
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Best Local
The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                             New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial meningitis; pneumonia; sepsis; otitis ear infection; antiinflammatory; antibacterial; auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masignani V, Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae type 4 strain
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(GENO-) INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                                                              SEQ ID
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LFLSNSFL 14
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                                                                                                                                                                                                                                                                                                                                                              942; 56pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                              English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        media;
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RESULT 14
ABG05253
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in develoy vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 249 proteins expressed by the identified coding regions from the
                                                       Claim 20; SEQ
                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                             N-PSDB; AAS69440.
                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the
                                                                                    biodiversity
                                                                                                                                                                          WPI; 2001-639362/73
                                                                                                                                                                                                        Drmanac
                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                           11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #5244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG05253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic sequence.
Note: The sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         where the first primer is substantially complementary to the target
                                                                                                                                                                                                                                     (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
                                                                                                                                                                                                        RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVSTYLFLSRQFL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LASEFLFLSNSFL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                     INC.
                                                     ID No 35612; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.5%;
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in developing
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chrome

for chromosome

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CC and gene mapping, and in recombinant production of (II). The colorities are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC specification, but was obtained in electronic format directly from WIPO careful activity and the printed content of the product of the printed content of the p
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention
                                                                                                                                                                                                                                                                                                                                     New isolated nucleic a genes from Drosophila interactions -
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N-PSDB; ABL07147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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11-JUL-2000; 2000US-0614150.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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251 DVNSEMLWYQNSFL
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ProDom; PD000425; TF_Fork_head; 1.
SMART; SM00339; FH; 1.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Porkhead box protein F1 (Forkhead-related pro-
related transcription factor 1) (FREAC-1) (Hey
forkhead homolog 8) (HFH-8).
FOXF1 OR FOXF1A OR FKHL5 OR FREAC1 OR HFH8.
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PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00658; FORK HEAD 2; 1.
PROSITE: PS00658; FORK HEAD 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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"Members of the HNP-3/forkhead family of transcription exhibit distinct cellular expression patterns in lung a the surfactant protein B promoter.";
Dev. Biol. 166:195-209(1994).
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Hellqvist M., Mahlapuu M., Samuelsson L.,
"Differential activation of lung-specific
proteins, FREAC-1 and FREAC-2.";
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Mammalia; Eutheria;
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                                                                                                                                               GO:0030324; P:lung development; IMP. GO:0009887; P:organogenesis; IMP. GO:0001570; P:vasculogenesis; IMP. erPro; IPR001766; TF Fork_head. mg. PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 fork-head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: LUNG AND PLACENTA. DOMAIN: ACTIVATION DOMAINS C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267:201-211(2001).
FUNCTION: PROBABLE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORKHEAD DOMAINS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIFIC GENES
                                                                                                                                                                                                                                                                                  MGI:1347470; Foxfla.
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                                                                                                                                                                                                                                                                                                                                                          U42556; AAC52445.1; -.
L35949; AAA64885.1; ALT_INIT.
AF346834; AAK35051.1; -.
                                                                                                                                                                                                                                                                                                                                          Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM .N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271:4482-4490(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NECESSARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAL OF (AND DISTINCT FROM) TRANSCRIPTIONAL ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enerbaeck S., Carlsson
genes by two forkhead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein FKHL5) (Forkhead-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Hepatocyte nuclear
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RESULT 3
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DNA BIND
CONFLICT
                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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EMBL; U13219; AJ
EMBL; AF085343;
                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: PROBABLE TRANSCRIPTI
SPECIFIC GENES.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- TISSUE SPECIFICITY: LUNG AND E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=98443197; PubMed=9769171;
Mahlapuu M., Pelto-Huikko M., Aitola M., Enerback S., (
Mahlapuu M., Pelto-Huikko M., Aitola M., Enerback S., (
Mahlapuu M., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Forkhead box protein F1 (Forkhead-related protein FKHL5) (Forkhead-related transcription factor 1) (FREAC-1) (Forkhead-related activator-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding site specificity and DNA bending."; EMBO J. 13:5002-5012(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hellqvist M., Mahlapuu M., Samuelsson L., "Differential activation of lung-specific proteins, FREAC-1 and FREAC-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q12946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pierrou S., Hellqvist M., Samuelsson L., Enerbaeck S., "Cloning and characterization of seven human forkhead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95045392; PubMed=7957066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: LUNG AND PLACENTA.

DOMAIN: ACTIVATION DOMAINS C-TERMINAL OF (AND DISTINCT FROM)
FORKHEAD DOMAINS ARE NECESSARY FOR TRANSCRIPTIONAL ACTIVATION
SIMILARITY: Contains 1 fork-head domain.
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22 113 1
7 19 (
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                       AAC50399.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTION
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AGEYPHDSSVPASPILLPAGAGGVMEPHAVYSSSAAAWPPA
-> GRGVPAPRQLGARFTAARPAPAESWSRTPFTPALQQPG
RP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P (IN REF. 2).
046AE0D8D1765A69
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enerbaeck S., Carlsson genes by two forkhead
                                                                                                                                                                                                                                                                                                                                                                                                                                  FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carlsson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activation
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                                                                                                                                                                                                      a collaboration
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EMBL; AF085342; AAC61576.1; JOINED HSSP; Q63245; 2HFH.

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Best Local
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Forkhead box protein F2 (Forkhead-related protein FKHL6) (Forkhead-related transcription factor 2) (FREAC-2) (Forkhead-related activator)
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Genew; HGNC:3809; FOXF1.
MIM; 601089; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005657; C:transcription factor complex;
GO; GO:0005515; F:protein binding activity; TAS.
InterPro; IPR001766; TF Fork_head.
Pfam; PF00250; Fork head; 1.
PRINTS; PR00053; FORKHEAD.
ProDom; PD000425; TF Fork_head; 1.
SMART; SM00339; FH; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSO0658; FORK_HEAD_1; 1.

PROSITE; PS00658; FORK_HEAD_2; 1.

PROSITE; PS00658; FORK_HEAD_3; 1.

DNA-binding; Nuclear pTotein; 3; 1.

DNA-binding; Nuclear pTotein; Transcription regulation; Activator.

DNA_BIND 22 113 FORK-HEAD.

SEQUENCE 354 AA; 38034 MW; DC32373A7AD034EF CRC64;
            MEDLINE=98389768; PubMed=9722567;
Hellqvist M., Mahlapuu M., Blixt A.,
"The human forkhead protein FREAC-2
                                                                                   PARTIAL SEQUENCE FROM N.A.
MEDLINE=95045392; PubMed=7957066;
Pierrou S., Hellqvist M., Samuelsson L., Ener
Pierrou G., Hellqvist M., Samuelsson L., Ener
"Cloning and characterization of seven human
binding site specificity and DNA bending.";
EMBO J. 13:5002-5012(1994).
                                                                                                                                                                                        "Hellqvist M., Mahlapuu M., Samuelsson L., 
"Differential activation of lung-specific 
proteins, FRBAC-1 and FRBAC-2.", 
J. Biol. Chem. 271:4482-4490(1996).
                                                                                                                                                                                                                                                                                                         MEDLINE-99017977; PubMed-9799607;
Blixt A., Mahlapuu M., Bjursell C., Darnfors C.; Johannesson T.,
Enerbaeck S., Carlsson P.;
"The two-exon gene of the human forkhead transcription factor FREAC-2
(PKHL6) is located at 6p25.3.";
Genomics 53:387-390(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                              TISSUE=Lung;
MEDLINE=96224034; PubMed=8626802;
                                                                                                                                                                                                                                                                               SEQUENCE OF 37-444 FROM
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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9; Conserv
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, Enerbaeck S., Carlsson P.; contains two functionally teracts with TBP and TFIIB.";
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5.3;
                                                                                                                                 Enerbaeck S.,
                                                                                                                                                                                                                    Enerbaeck S.,
genes by two
                                                                                                                    forkhead
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                                                                                                                  proteins:
                                                                                                                                 Carlsson
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                                                                                                                                                                                                                                    Carlsson P.;
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RESULT 5
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DP54079; Q9J128;

101-CCT-1996 (Rel. 34, Created)

1128-FEB-2003 (Rel. 41, Last sequence update)

1128-FEB-2003 (Rel. 41, Last annotation update)

1128-FEB-2003 (Rel. 41, Last annotation update)

1128-FEB-2003 (Rel. 41, Last annotation update)

1128-FEB-2003 (Rel. 41, Last motation update)

1128-FEB-2003 (Rel. 41, Last sequence update)
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PROSITE;
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00053; FORKHEAD.
ProDom; PD000425; TF Fork_head;
SMART; SM00339; FH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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-I- FUNCTION: PROBABLE TRANSCRIPTION ACTIVATOR FOR A NUMBER OF LUNG-
                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001766; TF Fork_head.
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005667; C:transcription factor complex; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:3810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>
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TISSUE SPECIFICITY: LUNG AND PLACENTA.
DOMAIN: TWO ACTIVATION DOMAINS, AD1 AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 fork-head domain.
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PS00658; FORK HEAD 2; 1.
PS50039; FORK HEAD 3; 1.
ing; Nuclear protein; Tra
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POLY-SER.
POLY-SER.
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POLY-GLY.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-HIS
                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription
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6.7;
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ng as its content is in no
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                                                                                                                                                                                    (Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulation; Activator.
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EMBL; AF268970; AAF823772.1; J-
EMBL; AF268970; AAF82772.1; JI
EMBL; AF268971; AAF82772.1; JI
EMBL; AF268972; AAF82772.1; JI
EMBL; AF268973; AAF82772.1; JI
EMBL; AF268974; AAF82772.1; JI
EMBL; AF268974; AAF82772.1; JI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; Provers, DNAPOLIG.

PRINTS; PRO0867; DNAPOLIG.

SMART; SM00482; POLAC; 1.

PROSITE; PS00447; DNA POLYMERASE A; 1.

PROSITE; PS00447; DNA POLYMERASE; DNA replication;

Transferase; DNA-directed DNA polymerase; DNA replication;

Magnesium.

**Comparing the comparison of the com
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InterPro; IPR001098; DNA pol.
InterPro; IPR002297; DNA polG.
Pfam; PF00476; DNA pol A; 1.
PRINTS; PR00867; DNAPOLG.
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                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c; TISSUE=Muscle; Chang S.W., Colvin S., Sarkos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mott J.L., Denniger G., Zullo S.J., Zassenhaus "Genomic structure of murine mitochondrial DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20514044; PubMed=11058962;
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SUBCELLULAR IOCATION: Micochondrial.
SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell Biol. 19:601-605(2000).
FUNCTION: INVOLVED IN THE REPLICATION
CATALYTIC ACTIVITY: N deoxynucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
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VDLAEEFLLTDNS
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Q -> K (IN REF.
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JOINED.
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B -> D (IN REF. 1)
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                                                                          Mismatches
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triphosphate = N diphosphate
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polymerase-gamma.";
                                                                                                            Length 1239;
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Browks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Leather S., Mollett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Gliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowiisch E.,
RA Gulier K., Gutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Modward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer B., Moester D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer B., Moester M., Bohl T.M.,
RA Gabel C., Fuchs M., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Benito J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gel Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Morseno S., Armstrong J., Forsburg S.L.,
RA Cartnitt I., Link G., Mickeller H., Wandler H., Purneller B.,
RA Cartnitt I., Link G., Mickeller H., Wandler H., Purneller B.,
RA Cartnitt I., Link G., Mickelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97282620; PubMed=9136929;
Shieh J.C., Wilkinson M., Buck V., Morgan B., Makino
Millar J.B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Po
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe."
Nature 415:871-880(2002).
                                                                       MEDLINE=97331762; PubMed=9188094; Shiozaki K., Shiozaki M., Russell P., Shiozaki M., Russell P., Wide and the fission "Mc94 mitotic catastrophe suppressor regulates the fission cycle through the Wik1-Wis1-Spc1 kinase cascade."; Mo1. Biol. Cell 8:409-419(1997).

-i- FUNCTION: INVOLVED IN A.SIGNAL TRANSDUCTION PATHWAY THE
                                                                                                                                                                                                                                                                                                                                                                                                                               Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The Mcs4 response regulator coordir activated Wak1-Wis1-Sty1 MAP kinase
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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   FUNCTION: INVOLVED IN A SIGNAL TRANSDUCTION PATHWAY THAT IS ACTIVATED IN UNDER CONDITIONS OF HEAT SHOCK, OXIDATIVE STRESS OR LIMITED NUTRITION. UNLIKE WIN1, IT IS NOT ACTIVATED BY CHANGES IN
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RESULT 7
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R PRINTS; PR00109; TYRKINASE.

R PRODOM; PD000001; Prot_kinase; 1.

R PROSITE; PS00107; PROTEIN_KINASE_DM; 1.

R PROSITE; PS50011; PROTEIN_KINASE_DM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_DM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

TATABSE PROSITE; PS00108; PROTEIN_KINASE; ATP-binding.

TOMAIN 1037 1306 PROTEIN KINASE; ATP-binding.

TOMAIN 1043 1051 PROTEIN KINASE; ATP-binding.

TOMAIN 1051 PROTEIN KINASE PROTEIN KINASE; ATP-binding.
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EMBL; Y07750; CAA69030.1; ALT_INIT.

EMBL; Y11989; CAA72718.1; -.

EMBL; U11989; CAA72718.1; -.

EMBL; U1521; AAB39762.1; -.

PIR; T39225; T39225.

HSBP; P24941; ICKP.

GeneDB_SPombe; SPAC9G1.02; -.

InterPro; IPR000719; Prot kinase.

InterPro; IPR001249; Tyr_bkinase.

Pfam; PB001649; Tyr_bkinase.
"Nucleotide Bequest:
a quail mitochondrial genome.";
J. Mol. Evol. 32:153-161(1991).
-I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol
-I- CATALYTIC BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
                                                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.
MTND1 OR ND1 OR NADH1.
Coturnix coturnix japonica (Japanese quail).
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BINDING
ACT SITE
CONFLICT
CONFLICT
                                                                                             SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=91178819; PubMed=1706782;
Desjardins P., Morais R.;
"Nuclectide sequence and evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                      Archosauria; Aves;
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                                                                                                                                                                                                                                                                      Mitochondrion.
                                                                                                                                                                                                  NCBI_TaxID=93934;
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RL -> SP (IN REF. 3).
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; Galliformes; Phasianidae; Phasianinae;
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047492;
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                                                                                           Prodom; PD0022107; NADH dh ubiql; 1.

Oxidoreductase; NAD; Ubiquinone; Mitochondrion
Oxidoreductase; NAD; Ubiquinone; Mitochondrion
Oxidoreductase; NAD; Ubiquinone; Mitochondrion
                                                                                                       Pfam; PF00420; oxidored q2; 1.
Pfam; PF00420; oxidored db ubiq; 1.
Phonography of continue; Mitochondrion
Phonography of continue; Mitochondrion
Phonography of continues; Mitochondrion
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                                                                                                                                                                PIR; T11886; T11886.
InterPro; IPRO03215; NADH dh ubiq1.
InterPro; IPRO01313; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
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InterPro; IPR001694; Resp_NADH_dh1.
Pfam; PF00146; NADHdh; 1.
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                                               Conservative
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RESULT 9 LSPA\_ENTAE ID LSPA\_E

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01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lipoprotein signal peptidase (EC 3.4.23.36) (
peptidase) (Signal peptidase II) (SPase II).
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TRANSMEM
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Isaki L., Kawakami M., Beers R., Hom R.,
"Cloning and nucleotide sequence of the I
peptidase II (1sp) gene.";
J. Bacteriol. 172:469-472(1990).
-!- FUNCTION: THIS PROTEIN SPECIFICALLY (
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001872; SigPTase pfam; PF01252; Peptidase A8; I PRINTS; PR00781; LIPOSIGPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacter aerogenes (Aerobacter aerogenes).
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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HAMAP; MF_00161; -; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to peptidase family A8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diacylglyceryl group.
SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL PEPTIDES FROM PROLIPOPROTEINS.
CATALYTIC ACTIVITY: Cleavage of N-terminal leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane prolipoproteins. Hydrolyzes Xaa-Xbb-Xcc-|-Cys, in whice Xaa is hydrophobic (preferably Leu), Xbb is often Ser or Ala, is often Gly or Ala, and the Cys is alkylated on sulfur with a
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                                                                                                8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    PD004304; SigPTase A8; 1.
s; TIGR00077; lspA; 1.
; PS00855; SPASE II; 1.
se; Aspartyl protease; Tra
IDLGSKFLILQN 33
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                                                                                                                      54.9%;
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                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
                                                                                                                        Pred.
                                                                                                                                       Score 39;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                             PERIPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Inner men
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                   A47A352CB1616724 CRC64;
                                                                                                  ed. No. 5.6;
Mismatches
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(See http://www.isb-sib.ch/announce/
                                                                                                                                            DB 1;
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VARIANT 20
VARIANT 26
VARIANT 26
VARIANT 30
VARIANT 45
VARIANT 51
VARIANT 51
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                                                                                                                                                                                        InterPro; IPR003918; NADHub_o:
InterPro; IPR001750; Oxidored
Pfam; PF00361; oxidored_q1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANTS GLY-11 CYS-45; SER-51; SER-61; GLY-64; VAL-76 CSTRAIN-8B1, AB2, Brietol N2, CB4852, CE CB4857, CB4858, KR314, PB303, PB306, RW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Ascaris suum.";
Genetics 130:471-498(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92201635; PubMed=1551572;
Okimoto R., Macfarlane J.L., Clary D.O.,
"The mitochondrial genomes of two nematoo
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15-SEP-2003 (Rel.
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MEDLINE=92201635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol. Evol. 20:393-400(2003).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22531585; PubMed=12644560;
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    42, Last annotation update)
oxidoreductase chain 4 (EC 1.6.5

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RW7000, and TR403;
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des, Caenorhabditis
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    PB306).
PB306).
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RESULT 11
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16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation updat
Acid phosphatase surE (EC 3.1.3.2).
SURE OR TC0491.
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                                                                                                               EMBL; AB002318; AAF39336.1; ALT_INIT.
HSSP; P96112; 1J9L.
TIGR; TC0491; -.
HAMAP; MF_00060; -; 1.
InterPro; IPR002828; SurE.
Pfam; PF01975; SurE; 1.
ProDom; PD005378; SurE; 1.
                                                                                                                                                                                        use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                 MEDLINE 2015 0255; PubMed=10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., White O., Hickey E.K., Peterson J., Utterbab, Linher K., Weldman J., Khouri H., Craven B., Gwinn M., Nelson W., DeBoy R., Kolonay J., McEisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia muridarum.
Bacteria; Chlamydiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SURE CHLMU
                                                                                                                                                                                                                                                                                                                          "Genome sequences of Chlamydia trachomatis MoPn and pneumoniae AR39.";
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                                                                                                         TIGRFAM8;
                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM
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                                        PD005378; SULL,
B; TIGR00087; BUTE; 1.
B; TIGR00087; BUTE; 1.
Be; Magnesium; Complete proteome.
MAGNESIUM (BY
15 15 MAGNESIUM (B)
47 47 MAGNESIUM (B)
105 105 MAGNESIUM (B)
1077 POTENTIAL.
  6; Conserv
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8; Conserv
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          53.5%;
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L -> V (IN STRAIN PB306).
G -> S (IN STRAIN PB303).
SAPLVLMMYNVFWLSVFY -> QHH (KR314).
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                                        80E5A79A0B4F792E CRC64;
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Utterback T., Berry
raven B., Bowman C.,
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                                                                                                                                                                                                                                                                                                                                    Chlamydia
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y K., Bass S.,
, Dodson R.,
, Salzberg S.L.,
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   RESULT
TRME_LE
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                                                     HAMAP; MF 00379; ; 1.
InterPro; IPR005289; GTP-bindding_dom.
InterPro; IPR0052917; WMR HSR1.
InterPro; IPR005297; Small_GTP.
InterPro; IPR005225; Small_GTP.
InterPro; IPR004520; ThdF.
Pfam; PF01926; MMR_HSR1; 1.
PRINTS; PR00449; RASTRNSFRMNG.
tRNA processing;
NP_BIND 227
NP_BIND 274.
                            TIGRFAMS; TIGR00650; MG442; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
TIGRFAMS; TIGR00450; thdF; 1.
                                                                                                                               EMBL; AB001721; BAA19450.1;
EMBL; AB010203; BAA24373.1;
EMBL; AE011208; AAN47379.1;
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P97043;
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                                                                                                                        EMBL; AE01120
PIR; T00126;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Spirochaetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRME OR LA0180.
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interrogans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
 GTP-binding; Complete proteome 234 GTP (POTENTIAL). 278 GTP (POTENTIAL).
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MEDLINE=22598143; PubMede12712204;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu.-P., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
                                                                                use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            Nature 422:888-893(2003).

-I- FUNCTION: EXHIBITS A VERY HIGH INTRINSIC GTPASE HYDROLYSIS RUINOLVED IN THE BIOSYNTHESIS OF THE HYPERMODIFIED NUCLEOSIDE METHYLAMINOMETHYL-2-THIOURIDINE, WHICH IS FOUND IN THE WOBBLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takahashi Y., Akase K., Hirano H., Fukunag "Physical and genetic maps of the Leptospi icterohaemorrhagiae strain Ictero No. 1 chickerohaemorrhagiae strain Ictero No. 1 chickerohaemorrhagiae strain Ictero No. 1 chickeroh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Ictero NG.1 / Serogroup Ic
MEDLINE=98332717; PubMed=9666070;
                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing.";
                                                                                                                                                                                                                                                                                         proteins. TrmE subfamily.
                                                                                                                                                                                                                                                                                                              POSITION OF SOME TRNAS (BY SIMILARI'S SIMILARITY: Belongs to the era/trmE
                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLSDEYLALANNYI 239
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation updat
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ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 chromosome and sequencing
the 5S rRNA gene.";
                                                                                                                                                                                                                                   is produced through
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                                                                                                                                                                                                           collaboration -
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FT
                                                                                                                                                                                                                                                                                                                                                                                      RA James K., Jones M., Deather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gorzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sancheź M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Usesery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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01-OCT-1996
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YQ37_s
                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
Hypothetical
SEQUENCE 7:
                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the company of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein SPCC188.07.
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(Rel. 41, Last annotation update)
l protein C188.07 in chromosome II
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Pred. No. 24;
3; Mismatches
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14193682700A2634 CRC64;
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                                                                                                                                                                                                                                                                                                                  a collaboration war. outstation -
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P55196; O75087; O75
01-OCT-1996 (Rel. 4
16-OCT-2001 (Rel. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P55196-3; Sequence=VSP_000219, VSP_000220;

-!- DISEASE: Involved in acute leukemias by a chromosomal translocation t(6;11)(q27;q23) that involves MLLT4 and MLL/HRX.

The result is a rogue activator protein.

-!- SIMILARITY: Contains 1 dilute domain.
-!- SIMILARITY: Contains 1 FHA domain.
-!- SIMILARITY: Contains 1 FHA domain.
-!- SIMILARITY: Contains 1 FHA domain.
-!- SIMILARITY: Contains 2 Ras-associating domains.
-!- SIMILARITY: Contains 2 Ras-associating domains.
-!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
-- WWW="http://www.infobiogen.fr/services/chromcancer/Genes/AF6.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94061833; PubMed=8242616;
Prasad R., Gu Y., Alder H., Nakamura T., Canaani Ö., Saito H.,
Prasad R., Gu Y., Alder H., Nakamura T., Canaani Ö., Saito H.,
Huebner K., Gale R.P., Nowell P.C., Kuriyama K., Miyazaki Y.,
Croce C.M., Canaani B.;
"Cloning of the ALL-1 fusion partner, the AF-6 gene, involved in
acute myeloid leukemias with the t (6;11) chromosome translocation.";
Cancer Res. 53:5624-5628(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic structure, DNA perioring of the human AF-6 gene.";
DNA Res. 5:115-120(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minami M., Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98344142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                          Name=3
                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic (Probable). ALTERNATIVE 'PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245
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; 075088; 075089; Q9NU92;
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ima M., Shirahama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                  splicing; Named isoforms=3
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Pred. No.
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RESULT 15
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InterPro; IPR00273; PHA.
InterPro; IPR001478; PA.
InterPro; IPR00159; RA.
InterPro; IPR00159; RA.
InterPro; IPR00159; RA.
Pfam; PF01843; DIL; 1.
Pfam; PF00498; PHA; 1.
Pfam; PF00595; PDZ; 1.
Pfam; PF00595; PDZ; 1.
SMART; SM00224; PHA; 1.
SMART; SM00224; PFA; 1.
SMART; SM00234; PDZ; 1.
SMART; SM00234; PDZ; 1.
SMART; SM00316; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
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EMBL; AB011399; BAA32483.1; -.
EMBL; AB011399; BAA32485.1; -.
EMBL; U02478; AAC50059.1; -.
EMBL; AL049698; CAB76850.1; -.
HSSP; Q12923; 3PDZ.
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GO:0005911; C:intercellular junction; TAS.
GO:0008022; F:protein C-terminus binding activity; TAS.
GO:0007155; P:cell adhesion, TAS.
GO:0007267; P:cell adhesion, TAS.
GO:0007267; P:cell-cell signaling; TAS.
GO:0007048; P:oncogenesis; TAS.
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                                                                              Similarity
8; Conserv
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2; Mismatches
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                                                                                                                                                           isoform 3).
/FTId=VSP 000219.
Missing (In isoform ?
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Missing (in isoform 1).
/FTId=VSP_000218.
                                                                                                                                                                                          ICRPPLPRDYEPPSPSPAPGAPPPPPQRNASYLKTQVLSPD
SLFTAKFVAYWEEEBEEDCSLAGQDKYSSTRKSHGDL ->
PNSYPGSTGAAVGAHDACRDAKEKRSGDADSPGSSGAPE
NLTFKERQRLFSQGQDVSNKVKASRKLTELENELNTK (in
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PILASACFPWG (in 1soform 1).
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         PRT;
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> DSSHFD (IN REF. 3).
> DV (IN REF. 1).
> P (IN REF. 1).
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> P (IN REF. 1).
EB1FE7F04879CE8F CRC64;
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28-FEB-2003
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RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Brom S.,
RA Browillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Chis S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chis S.K., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Gallaron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moseri D., Nakai S., Noback M.,
RA Monne D., O'Railly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Raeuchi M., Tamakoshi A., Tarakahashi H., Takamaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                 "Characterization of the pcp gene peptidase of Bacillus subtilis."; FEBS Lett. 305:67-73(1997)
This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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MEDLINE=98044033;
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                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92339527; PubMed=1353026; Awade A., Cleuziat P., Gonzales T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 190-245 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256(1997).
                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein (Potential) SIMILARITY: BELONGS TO THE TATC FAMILY. CAUTION: REF. 1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 20.
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DR EMBL; Z99105; CAB12058.1; -.

DR EMBL; X66034; -; NOT_ANNOTATED_CDS.

DR PIR; D69754; D69754.

DR Subtilist; BG11175; ycbT.

DR InterPro; IPR002033; Translocase.

P fam; PF00902; TatC; 1.

DR PROSITE; P80121218; TATC; 1.

ET TRANSMEM 60 80 POTENTIAL.

FT TRANSMEM 110 130 POTENTIAL.

FT TRANSMEM 191 211 POTENTIAL.

FT TRANSMEM 191 211 POTENTIAL.

FT TRANSMEM 212 232 POTENTIAL.

FT TRANSMEM 212 232 POTENTIAL.

FT TRANSMEM 212 332 POTENTIAL.

FT TRANSMEM 213 332 POTENTIAL.

FT TRANSMEM 2145 AA; 28114 MW; D5066B68056EC231 CRC64;

QUETY MATCh 52.1%; Score 37; DB 1; Length 245;

Best Local Similarity 53.3%; Pred. No. 19;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

DD 1 IDLASEFLFLSNSFL 15

DD 21 VTLAAFFLFLITAFL 35

Search completed: November 26, 2003, 12:31:20

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103.662 Million cell updates/sec
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   GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	51.4	52.1	52.1	52.1	52.1
346	342	294	293	251	249	172	166	164	164	164	705	1436	1210	1178	755
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B64976	T29192	E69817	G69954	G89928	C90526	A64168	AB0508	E85483	F90632	ZPECL	T49461	A99115	D88013	S78475	C90439
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## ALIGNMENTS

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A;Gene: GDB:FKHL5; FREAC1
A;Cross-references: GDB:450216; OMIM:601089
A;Map position: 16024-16024
C;Superfamily: unassigned fork head proteins;
F;6-97/Domain: fork head DNA-binding domain ho
                                                                                                                                                                                                                                                                            RESULT 2

$51624

$51624

$FREAC-1 protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 15-Uul-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999

C;Accession: $51624

R;Pierrou, S.; Hellqvist, M.; Samuelsson, L.; Enerbaeck, S.; Carlsson, P.

EMBO J. 13, 5002-5012, 1994

A;Title: Cloning and characterization of seven human forkhead proteins: binua; Reference number: $51624 MUID:95045392; PMID:7957066

A;Accession: $51624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-98 <BUS>
A;Cross-references: EMBL:L28920; NID:g1616966; PID:g456147; GSPDB:GN00001; MIPS:YAR053w C;Genetics:
C;Genetics:
A;Gene: MIPS:YAR053w
A;Cross-references: SGD:S0000085
A;Map position: 1R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabl submitted to the EMBL Data Library, February 1994
A;Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the A;Reference number: S53458
A;Accession: S53467
                                                                                                                                             A; Modlecule type: mRNA
A; Residues: 1-106 <PIE>
A; Cross-references: EMBL: U13219
C; Genetics:
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C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S53467
                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown
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Pred. No.
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     homology <FHD>
                                     fork head DNA-binding domain homology
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57.7%; 64.3%;

Score 41; DB 2; Pred. No. 2.6;

Length 106

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RESULT 5
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A;Map position: 16q24-16q24
C;Superfamily: unassigned fork head proteins; fork head DNA-binding F;6-97/Domain: fork head DNA-binding domain homology.
                           forkhead protein FREAC-2 - human (;Species: Homo sapiens (man) C;Date: 16-Jul-1999 #sequence_rev C;Accession: T09474
                                                                                                                                                                                                                                                                                                                                  A; Gene: HFH-8
C; Superfamilv:
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C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C;Accession: S51625
R;Pierrou, S.; Hellqvist, M.; Samuelsson, L.; Enerbaeck, S.; Carlsson, P. EMBO J. 13, 5002-5012, 1994
A;Title: Cloning and characterization of seven human forkhead proteins: bind A;Reference number: S51624; MUID:95045392; PMID:7957066
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dev. Biol. 166, 195-209, 1994

A;Title: Members of the HNF-3/forkhead family of transcription
A;Reference number: I49735; MUID:95046902; PMID:7958446
A;Accession: I49735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Clevidence, D.E.; Overdier, Dev. Biol. 166, 195-209, 1994
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C;Accession: I49735
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A; Residues: 1-106 < PIE>
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                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-376 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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A; Accession: S51625
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C;Species: Mus musculus (house mouse)
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Matches 9
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Best Local S
Matches
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                                            #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.G.; Peterson, R.S.; Porcella,
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Pred. No.
                                                                                                                                                                                                                                             Pred. No. 10;
L; Mismatches
                                                                                                                                                                                                                                                                            Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                           from GB/EMBL/DDBJ
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                                               11-May-2000
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                                                                               C;Accession: T39225
R;Churcher, C.M.; Gentles,
submitted to the EMBL Data
A;Reference number: Z21837
A;Accession: T39225
                                                                                                                                                                   MAP kinase kinase kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
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                               A;Molecule type: D
A;Residues: 1-1401
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S.; Barrell, Library, Aug

B.G.; Rajandream, ust 1997

M.A.;

Wood,

SCHO?

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A;Gene: GDB:PIGB
A;Cross-references: GDB:9956843; OMIM:604122
A;Map position: 15q21-15q22
C;Function:
A;Description: involved in surface protein binding to the membrane
A;Pathway: GPI-anchor biosynthesis
C;Keywords: 91ycosyltransferase; hexosyltransferase; transmembrane
E;60-77/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Takahashi, M.; Inoue, N.; Ohishi, K.; Maeda, Y.; Nakamura, N.; Endo, Y.; Fujita, T. EMBO J. 15, 4254-4261, 1996
A;Title: PIG-B, a membrane protein of the endoplasmic reticulum with a large lumenal A;Reference number: S71751; MUID:97015126; PMID:8861954
A;Accession: S71751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (EC 2.4.1.130) PIGB - h N;Alternate names: membrane protein PIG-B; phosphatidyl-inositol glycolipid biosynthesi: C;Species: Homo sapiens (man) C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002 C;Accession: S71751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: may function as transcription activator C;Superfamily: transcription factor HNF-3; fork head DNA-binding F;100-191/Domain: fork head DNA-binding domain homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Hellqvist, M.; Mahlapuu, M.; Blixt, C.; Enerback, S.; Carlsson, J. Biol. Chem. 273, 23335-23343, 1998
A;Title: The human forkhead protein FREAC-2 contains two functional protein contains two functional protein contains two functional protein contains two functional protein contains two functional proteins. 216682; MUID:98389768; PMID:9722567
A;Accession: T09474
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-444 <HEL>
A;Cross-references: EMBL:U13220; NID:g3425849; PID:g3425850
                                                                                                                                                                                                                                                                                             A;Note: part of the C;Genetics:
                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: D42138; A; Experimental source: cell line
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Similarity 9; Conser
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75.0%;
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64.3%;
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  Pred. No. 23;
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                                              Score 40;
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Pred. No.
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A; Map position: 1
C; Superfamily: unassign
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                                                                                                                                                                                                                                                                                                                                                                                                                        NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - sea anemone (Metridium senile) C;Species: mitochondrion Metridium senile (brown sea anemone, frilled sea anemone) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002 C;Accession: T11886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
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A; Residues: 1-72 < DES>
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J. Mol. Evol. 32, 153-161, 1991
A;Title: Nucleotide sequence and evolution
A;Reference number: S25422; MUID:91178819;
A;Accession: S25422
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A; Residues: 1-99 <BEA>
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                                                          Query Match
Best Local S
Matches 8
                                                                                                                                       Superfamily: NADH dehydrogenase (ubiquinone) chain 4L; (Keywords: membrane-associated complex; mitochondrion; NAD; oxidative
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se: strain 972h-; cosmid c9G1
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T12408
TNADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 -
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 -
C:Species: mitochondrion Heterorhabditis hepialus
C:Species: mitochondrion revision 23-Jul-1999 #text
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                                                                                                                                                          A;Start codon: TTG
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion
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A;Note: the authors translated
                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-25 < OK2>
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A;Title: Evidence for the frequent use of TTG as the translation initiation codon of mit A;Reference number: S13139; MUID:91045077; PMID:2235493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-409 < OKI >
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A;Title: The mitochondrial genomes of two nematodes, Caenorhabditis elegans A;Reference number: S26014; MUID:92201635; PMID:1551572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Caenorhabditis elegans mitochond (Species: mitochondrion Caenorhabditis elegans C;Species: mitochondrion Caenorhabditis elegans C;Date: 12-Feb-193 #sequence_revision 12-Feb-193 #text_change 03-Jun-2002 C;Accession: S26033; S25806
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A;Experimental source: strain BOD
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A; Accession: T12408
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A;Accession: $25806
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A;Note: the authors translated the initiation codon TTG for residue 1 as
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                                                                                                                                                            NAD; oxidative
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Ascaris

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RESULT 14
T18427
                                                                         R;Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, August 1997
                                                                                                               hypothetical protein C0335c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18427
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A;Introns: 65/2; 146/2; 222/1; 264/1; 304/3; 345/3; 435/3; 500/2; 834/3; 913/2; 977/3; 1
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ZC412.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
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                               A; Reference number: A; Accession: T18427
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A;Status, preliminary; translated from GB/EMBL/DDBJ
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A;Accession: T40798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z78067; PIDN:CAB01533.1; GSPDB:GN00023; CESP:ZC412.
A;Experimental source: clone ZC412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Residues: 1-1170 <WIL>
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;Residues: 1-819 <BEC>
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Job time :

15.9157

secs

Search completed: November 26, 2003, 12:36:06

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C;Species:
C;Date: 03-
C;Accession
                                                                                                                                                     A;Cross-references: GB:AE005672; PIDN:AAK74693.1; PID:gl4972010; GSPDB:GN00164; TIGR:SPA;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                           on, J.D.; Umayam, L.A.; Wnson, T.; Hickey, E.K.; HScience 293, 498-506, 200 A; Authors: Loftus, B.J.;
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D95062
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A;Residues: 1-3724 <LAW>
A;Residues: 1-3724 <LAW>
A;Cross-references: EMBL:Z98547; NID:e1325376; PID:e1325379; PIDN:CAB11104.1 C;Genetics: A;Introns: 307/1; 1545/2 A;Note: C0335c
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                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <KUR>
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                                                                                                                                       A;Gene: SP0536
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A;Accession: D95062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity protein BlpL [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Streptococcus pneumoniae;Date: 03-Aug-2001 #text_change 03-Aug-2001;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001;Accession: D95062
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9eq
    SPTREMBL 23:*

1: Sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate

6: sp_manmal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*
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 16 QBF570
17 Q9HJK3
10 Q9SRT3
17 Q9P9M6
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13 Q9PV9
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Q8wi47 gyrocarpus
Q9pv9 gallus gall
Q9pv9 gallus gall
Q9gv9 hernandia n
Q9w707 xenopus lae
Q9w706 xenopus lae
Q9w708 mus musculu
Q63861 heterorhabd
Q63862 heterorhabd
Q63860 heterorhabd
Q63863 streptococc
Q9hfu7 pneumocysti
Q54977 streptococc
                                                                                                                                     Q8f570 leptospira
Q9hjk3 thermoplasm
Q9srt3 arabidopsis
Q979m6 thermoplasm
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45	44	43	42	41	40	39	38	37	36	35	<u>د</u>	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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Q9vp08 drosophila	Q8aw25 brachydanio	Q9aka8 rickettsia	Q9etk8 streptococc	Q8bng5 mus musculu	$\sigma$	•	O77320 plasmodium	Q8idm0 plasmodium	Q23310 caenorhabdi	Q9pte5 xenopus lae	O94254 schizosacch	Q8sex3 coturnix co	Q9css4 mus musculu	Q9rf47 klebsiella		O63933 heterorhabd	O63858 heterorhabd	O63859 heterorhabd	O63932 heterorhabd	met	Q92521 homo sapien	Q8wvn7 homo sapien	N	ש	,_		Q9fb04 streptococc	O85731 streptococc

## ALIGNMENTS

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RESULT 1
Q8F570
ID 708F5
AC 08F5
AC 08F5
AC 10-M
DT 01-M
DT 01
RESULT 2
Q9HJK3
ID Q9HJ
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O1-MAR-2001 (TrEMBLrel. 16, L:
O1-MAR-2001 (TrEMBLrel. 16, L:
NADH dehydrogenase, chain J r
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Q8F570; O1-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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Ren S.;

Ren S.;

ARP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AE011357; AAN49015.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 53 AA; 6215 MW; BFF5A0A8134D8719 CRC64;
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Bacteria; Spirochaetes;
NCBI_TaxID=173;
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STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
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83.3%;
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                               Created)
Last sequence update)
Last annotation update)
related protein.
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Last annotation update)
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RESULT
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Best Local S
Matches 10
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Q9SRT3;
01-MAY-2000
"Arabidopsis Open Reading Frame (ORF) Clones.", Submitted (AUC-2002) to the EMBL/GenBank/DDBJ dEMBL; AC009853; AAF02144.1; -...
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D., Yamada K., Banh J., Chang C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

"Full Length CDNA of gene At3g07330 (GI:15231448).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
F2103.4 protein (Hypothetical protein).
F2103.4 OR AT3G07330.
F2103.4 OR AT3G07330.
F2103.4 OR AT3G07330.
F2103.5 Protein (Hypothetical protein).
F2103.6 Protein (Hypothetical protein).
F2103.7 Protein (Hypothetical protein).
F2103.8 Protein (Hypothetical protein).
F2103.9 Protein (Hypothetical
                                                                                                                           Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hsuan V.W., Lee J.M., Quach H.L., Tang C., Toriumi M., Wallender E.K., Wong C., Wu H.C., Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnst Bowman C.L., White O., Nierman W.C., Fraser C.M.; White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III BAC F2103 genomic submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 82 AA; 9081 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
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STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
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EMBL; AL445066; CAC12093.1;
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|IILASEFLFIGASFI
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                                                                                                                                                                                                                                                                                                                                                                       gth cDNA of gene At3g07330 (GI:15231448)."; (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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0.93;
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der E.K., Wong C.,
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Barnstead
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RESULT 5
QBWI47
ID QBWI
AC QBWI
DT 01-M
DT 01-M
DT 01-G
DB MATUR
GN MATUR
GO Chic
OC Euka
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CO Euka
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Matches
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Best Local
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                                                                                                                                                                Gyrocarpus americanus.
Chloroplast.
Chloroplast.
Eukaryota; Viridiplantae; S
Spermatophyta; Magnoliophyt
NCBI TaxID=63807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-GSS1 / DSM 4299 / JCM 9571;
Kawashina T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawashina-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kaw Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by genousequence of Thermoplasma volcanium.";
"---- Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
                                                                                                                                                                                                                                                                                                    01-MAR-2002
01-OCT-2002
Maturase K (
                                                                                                                                                                                                                                                                                                                                                                     Q8WI47
Q8WI47;
01-MAR-2002
                                                                                                                                                                                                                                                                                MATK.
                      "Slowly and rapidly evolving genes and phyloge angiosperms: an empirical assessment."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
                                                                                  Chatrou L.W.,
Chase M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NADH dehydrogenase I
TV1134 OR TVG1162541
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Pfam; PF00535; Glycos transf_2;

Hypothetical protein.

SEQUENCE 682 AA; 78371 MW; F
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Thermoplasmataceae; Thermoplasma.
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                                                                                                                                 SEQUENCE FROM
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2 (TrEMBLrel. 20, L
2 (TrEMBLrel. 22, L
(Intron maturase)
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                                                                                                           N.A.
Savolainėn
                                                                                                                                                                                             Magnoliophyta;
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                                                                                                        ٧.,
                                                                                                                                                                                             Streptophyta;
yta; Laurales;
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Last annotation updat
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Pred. No.
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                                                                                                           Σ.
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                                                                phylogeny
                                                                                                                                                                                             Embryophyta; Tracheophyta;
Hernandiaceae; Gyrocarpus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 82;
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                                                                                                             Bakker
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        CHLOROPLAST GROUP
                             databases
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                                                                                                                                                                                                                    Tracheophyta;
                                                                                                             Zanis
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                                                                              RESULT 7
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Best Local S
Matches 9
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Best Local (
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                 Q9GHV9
Q9GHV9;
01-MAR-2001
01-MAR-2001
01-OCT-2002
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9PVP9;
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                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Forkhead transcription factor (Fragment).
Gallus gallus (Chicken)
                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                          InterPro; IPR001766, TP Fork_head.
Pfam, PP00250; Fork_head; 1.
ProDom; PD000425; TF Fork_head; 1.
SMART; SM00339; FH; I.
                                                                                                                                                                                                                                                                                                       "Coelom formation: binary decision controlled by the ectoderm."; Development 126:4129-4138(1999).
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99387980; PubMed=10457021;
Funayama N., Sato Y., Matsumoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
mRNA processing; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP465295; AAL69409.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                  EMBL; AB028627; BAA84095.1; -. HSSP; Q63245; 2HFH.
        Intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTRONS (BY SIMILARITY)
                                                                                                            52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
         maturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conserv
                                                                                                                                                   Similarity
9; Conser
                                                                                                                                                                                                                     PS00658; FORK_HEAD_2; 1.
PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLFLSNSFV 73
                                                                                                                              IDLASEFLFLSNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLFLSNSFL 15
                                                                                                            IDPASEFMFEEGSF
                                                                                                                                                                                           295
295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
267 AA;
               (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                          PRELIMINARY;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
         (Maturase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.7%;
88.9%;
                                                                                                                                                                                         31829 MW; 7A05EE300CDA2839 CRC64;
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                                                                                                                                                            57.78;
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                                                                                                                                                            Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41;
Pred. No.
         (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5162C649702507C1 CRC64;
                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                           of the lateral plate mesoderm
                                                          360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295
                                                                                                                                                                       DB 13;
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RESULT 8
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Best Local S
Matches 8
                                                                                                Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel. :
XFD-13' protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic structure and embry helix factors XFD-13/13'.", submitted (JUN-1999) to the EMBL; AJ242679; CAB44731.1, HSSP; Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9W707
Q9W707
                                                                                                                                                                                                                                                               PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ247165; CAC05370.1; -.
InterPro; IPR000442; Intron maturse2
InterPro; IPR000666; MatK_N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matK sequences.";
Syst. Bot. 25:60-71(2000).
-!- FUNCTION: PROBABLY ASSISTS IN
                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00053; FORKHEAD.
ProDom; PD000425; TF Fork
SMART; SM00339; FH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA processing; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hernandia nymphaeifolia.
Chloroplast.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Laurales, Hernandiaceae, Hernandia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XFD-13'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Leaf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=121082;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001766; TF_Fork_head
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koester M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Toward a phylogenetic classification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLFLSNSFV
                                                                                                    Similarity
9; Conser
                                                                                                                                                                                                                                PS00657; FORK HEAD 1; 1.
PS00658; FORK HEAD 2; 1.
PS50039; FORK HEAD 3; 1.
372 AA; 40290 MW; 38
IDLASEFLFLSNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLFLSNSFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillinger K.,
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                               TF_Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.7%;
88.9%;
                                                                                                                                   57.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K., Knoechel W.;
embryonic expression of the Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12,
12,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last
Last
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                                                                                                    Score 41; DB
Pred. No. 34;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB Pred. No. 33;
                                                                                                                                                                                                                                       388089A07F1C25CC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the Lauraceae: Evidence from
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                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 360;
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                                                                                                                                                                  Length 372;
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                                                                                                       Indels
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IDPASEFMFEEGSF 143

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054743
                               ACCOMENTATION OF THE PROPERTY 
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Best Local S
Matches
Miura N., Kakinuma K., Sato M., Aiba N., Sugiyama T.
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databas
EMBL; Y12293; CAA72972.1; -.
EMBL; Y12294; CAA72972.1; JOINED.
EMBL; Y11294; CAA72972.1; JOINED.
EMBL; Y11294; CAA729735.1; -.
EMBL; Y11148; CAA72035.1; -.
HSSP; Q63245; 2HFH.
TRANSFAC; T02514; -.
RGD; MGI:1347479; Foxf2.
InterPro; IPR001766; TF Fork head.
InterPro; IPR001766; TF Fork head.
InterPro; IPR001766; TF Fork head.
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ProDom; PD000425; TF FORK head; SMART; SM00339; FH; I .

PROSITE; PS00657; FORK HEAD 1; 1

PROSITE; PS00658; FORK HEAD 2; 1

PROSITE; PS50039; FORK HEAD 3; 1

PROSITE; PS50039; FORK HEAD 3; 0

SEQUENCE 373 AA; 40357 MW; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Miura N.,
Submitted
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic structure and embryonic expression of Xenopus factors XFD-13/13'.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases EMBL; AJ242680; CAB44732.1; -.
HSSP; Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 11-446 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       054743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Koester M., Dillinger K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kenopus laevis (African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (enopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Kakinuma H.,
(APR-1997) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sato
o the
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB Pred. No. 34; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          M., Aiba N., Sugiyama T.;
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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040EEE7BAD63A896 CRC64;
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34;
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Best Local S
Matches 9
                                                                                                                                                                          PRINTS; EKVOULT; TF FORK_HEAU, -
PRODOM; PD000435; TF FORK_HEAU, -
SMART; SM00339; FH; I.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS00658; FORK_HEAD_3; 1.
PROSITE; PS50039; PSF0039; PSF00
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               063861;
SEQUENCE FROM N.A.
                                              NCBI_TaxID=52063;
                                                                                Mitochondrion.
Eukaryota; Metazoa;
Heterorhabditidae; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF066886; AAC19107.1;
InterPro; IPR001750; Oxidored q1.
Pfam; PF00361; oxidored q1; 1.
NAD; Oxidoreductase; Ubiquinone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu J., Berry R.E., Blouin M.S., "Molecular differentiation and g (rhabditidae) heterorhabditidae) Mitochondrial DNA.",
J. Parasitol. 85:709-715(1999).
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Heterorhabditidae; I
NCBI_TaxID=52063;
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164
164 AA;
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3 (TrEMBLrel. 07,
2 (TrEMBLrel. 22,
cogenase subunit 4
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18675 MW;
                                                                                      Heterorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heterorhabditis.
                                                                                                               Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematoda; Chromadorea;
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46.7%;
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Pred. No.
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Pred. No.
                                                                                                               Chromadorea;
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RESULT 14
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Q98650;
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RGG.
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NON_TER
SEQUENCE
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NAD; Oxidoreductaga. "TT"
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EMBL, AF066885; AAC19106.1; -.
InterPro, IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
NAD; Oxidoreductase; UbIquinone; Mitochondrion
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MEDLINE=99389049; PubMed=10461953;
Liu J., Berry R.E., Blouin M.S.;
"Molecular differentiation and phylogeny
(rhabditida: heterorhabditidae) based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99389049; PubMed-10461953;
Liu J., Berry R.E., Blouin M.S.;
"Molecular differentiation and phy
(rhabditida: heterorhabditidae) bar
witochondrial DNA.";
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Heterorhabditidae; I
NCBI_TaxID=52065;
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J. Parasitol. 85:709-715(1999).
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-MAY-2000 (TrEMBLrel.:
-MAY-2000 (TrEMBLrel.:
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7; Conserv
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164 AA;
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% 3Lrel. 07,
% 3Lrel. 22,
% 9 subunit 4
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Heterorhabditis.
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; Pred. No. 23;
3; Mismatches
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based on
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Search completed: November Job time : 34.7108 secs

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RESULT 15
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Nucleic Acids Res. 28
Nucleic Acids Res. 28
EMBL; AF291574; AAG1/
EMBL; AF291574; AA;
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Q9HFU7;
Q1-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
Ornithine decarboxylase a
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                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99184993; PubMed=10085009; Chaussee M.S., Ajdic D., Ferretti J.J.; The rgg gene of Streptococcus pyogenes extracellular SPE B production."; Infect. Immun. 67:1715-1722(1999). EMBL; AF091252; AAD23950.1; -. NON_TER 186 186
                                                                                                                                                                                  Eukaryota; Fu
Pneumocystis.
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NCBI_TaxID=1314;
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Bacteria, Firmicutes; Lactobacillales;
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190
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larity 53.3%;
Conservative
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AA; 27677 MW;
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Pred. No.
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of triplet decoding, which
is a sensor for an autoregu
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Result
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Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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Match Length
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pn2_6/ptodata/2/pubpaa/US09Ā PUBCOMB.pep:*
pn2_6/ptodata/2/pubpaa/US09E PUBCOMB.pep:*
pn2_6/ptodata/2/pubpaa/US090 NEW PUB.pep:*
pn2_6/ptodata/2/pubpaa/US10Ā PUBCOMB.pep:*
pn2_6/ptodata/2/pubpaa/US10Ā PUBCOMB.pep:*
pn2_6/ptodata/2/pubpaa/US10E PUBCOMB.pep:*
pn2_6/ptodata/2/pubpaa/US10C PUBCOMB.pep:*
pn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
pn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
pn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
pn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
  -6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:
6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
-6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:
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2 US-10-092-138-16

12 US-09-230-111C-16

3 US-08-681-219-7

3 US-08-681-219-25

10 US-10-092-138-23

12 US-10-092-138-23

12 US-09-230-111C-5

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12 US-09-230-111C-23

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12 US-09-230-111C-23

12 US-09-230-111C-23

12 US-09-230-111C-23

13 US-09-756-854-3

14 US-10-041-574-3
US-10-280-047-3
US-09-826-212-7
US-09-802-669-2
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              Sequence 18, Appl
Sequence 16, Appl
Sequence 17, Appli
Sequence 7, Appli
Sequence 25, Appli
Sequence 5, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 3, Appli
Sequence 7, Appli
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24	е 36,	O.	494, 1	e 202,	731, 1	e 843,	Sequence 570, App	e 142,	æ	e 142	æ	e 138	e 138,	æ	e 140,	e 140,	e 25,	е 3,	ω `	Sequence 7, Appli	e u	e 4	o 6,	<u>.</u>	٥	e 2,	4	20	Sequence 6, Appli

## ALIGNMENTS

US-08-681-219-18 ; Sequence 18, Application US/08681219 ; Publication No. US20020058607A1 APPLICATION NUMBER: US/08/681,219
FILING DATE: 22-UUL-196
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION UMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/48962/
TELECOMMUNICATION INFORMATION: GENERAL INFORMATION: APPLICANT: Takaak TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INPORMATION FOR SEQ ID NO; :18:
SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: APPLICANT: Takaaki Sato and Junn Yanagisawa
TITLB OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGP
TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND THE GLGP STREET: 1185 Aver CITY: New York STATE: New York NUMBER OF SEQUENCES: 3 COUNTRY: U.S.A. STRANDEDNESS: ADDRESSEE: LENGTH: 10036 amino acids 1185 Avenue of the Americas Cooper & Dunham LLP single 0575/48962/JPW/JKM

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                                                                                                            ; OTHER INFORMATION: Description of Artificial ; OTHER INFORMATION: Sequence:source:synthesized US-09-230-111C-16
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; Sequence 16, Application US/09230111C
; Publication No. US20030203414A1
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US-10-092-138-16
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CURRENT APPLICATION NUMBER: US/10/092,138
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
                                     Query Match
Best Local Similarity
Matches 15; Conserv
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publication No. US20030170723A1
GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
TITLE OF INVENTION: MIOCHEMICAL PROTEIN-PROTEIN INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                      APPLICANT: Yanagisawa, Junn
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOMAIN AND USES THEREOF
FILE REPERENCE: 48962-A-PCT-US
CURRENT FILING DATE: 1999-05-17
NUMBER: 05 SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, J
                                                                                                                                                                                                                                                           SOFTWARE: PatentIň Ver. 2.1
                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                 FEATURE:
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1 DSEMYNFRSQLASVV 15
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                                       Conservative
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                                                      100.0%;
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Pred. No. 3.7e-07;
                                                      Score 73; DB 12;
Pred. No. 3.7e-07;
                                       Mismatches
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US-08-681-219-25

Sequence 25, Application US/08681219

Publication No. US20020058607A1

GENERAL INFORMATION:
APPLICANT: Takaaki Sato and Junn Yanagisawa
ITILE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN

TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF

UMMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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Publication No. US20020058607A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 53.3%; les 8; Conservative
                      COUNTRY: U.S.A. ZIP: 10036
                                                                          CITY: New York
                                                                                                 STREET:
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                                                                                                                    ADDRESSEE:
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                                                          New York
                                                                                           E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1185 Avenue of the Americas
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VENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
VENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cooper & Dunham LLP
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Pred. No. 0
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MEDIUM TYPE:

Floppy disk

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RESULT 7
US-10-092-138-23
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Sequence 23, Application US/10092138

Publication No. US20030170723A1

GENERAL INFORMATION:
APPLICANT: Sato, Taka-aki
TITLE OF INVENTION: HETHOD OF PREPARING A PROTEIN ARRAY BASED ON
TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: 65823/JPM/PT
CURRENT FILING NOWBER: US/10/092,138
CURRENT FILING NATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON TITLE OF INVENTION: BICCHEMICAL PROTEIN-PROTEIN INTERACTION FILE REFERENCE: 65823/JPW/PT CURRENT APPLICATION NUMBER: U5/10/092,138 CURRENT FILING DATE: 2002-09-06 NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acide
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10092138
Publication No. US20030170723A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01
FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                    DSENSNFRNEIQSLV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taka-Aki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.2%;
                                                                                                                                                                                                                                                                                                                                                             56.2%; Score 41; DB 53.3%; Pred. No. 0.4;
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Pred. No.
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APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, Junn
ITILE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ
TITLE OF INVENTION: DOMAIN AND USES THEREOF
FILE REFERENCE: 48962-A-PCT-US
CURRENT APPLICATION NUMBER: US/9/230,111C
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 33
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 15
                                                                                                                                                                                                                                                                                                                             RESULT 9
US-09-230-111C-23
; Sequence 23, Application US/09230111C
; Publication No. US20030203414A1
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US-09-230-111C-5
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                                                                     APPLICANT: Sato, Taka-Aki
APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, Junn
ITTLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOMAIN AND USES THEREOF
FILE REFERENCE: 48962-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,111C
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 23
LENGTH: 15
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09230111C Publication No. US20030203414A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 23
LENGTH: 15
TYPE: PRT
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                                    ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:source:synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:source:synthesized
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Pred. No.
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RESULT 11
US-09-756-854-3
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TITLE OF INVENTION: Rapamycin Based Regulation of Biological Events
FILE REFERENCE: 345B PCT
CURRENT APPLICATION NUMBER: US/10/341,967
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US/09/481,620A
PRIOR APPLICATION NUMBER: US/09/481,620A
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 132
SOPTWARE: Patentin version 3.0
SEQ ID NO 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09756854
Patent No. US20020164684A1
GENERAL INFORMATION:
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Best Local Similarity 53...
Matches 8; Conservative
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Best Local Similarity
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NAME/KEY: PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 19
                                                                                                           COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
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APPLICATION NUMBER: 09/095,094
FILING DATE: <Unknown>
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                                                     APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: -Unknown>
                                                                                                                                                                                                                                                               STATE: MD
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                                                                                                                                                                                                                                                                                                                                                                                          Gentz, Reiner
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Pred. No.
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Pred. No. 0.
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                                                                                                                                Version #1.30
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                                                                                          RESULT 13
US-10-280-047-3
                                     GENERAL INFORMATION:
                                                        Sequence 3, Application US/10280047 Publication No. US20030180883A1
     APPLICANT: Ni, Jian APPLICANT: Rosen,
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RESULT 12
US-10-041-574-3
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PRIOR APPLICATION NUMBER: 09/527,236
PRIOR FILING DATE: 2000-03-16
PRIOR PPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR PPLICATION NUMBER: 09/095,094
PRIOR FILING DATE: 1998-06-10
PRIOR PRIOR DATE: 1998-06-10
PRIOR PPLICATION NUMBER: 60/126,019
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-05-14
                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 3
                                                                               Matches
                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION NUMBER: US/10/041,574
CURRENT FILING DATE: 2002-01-10
CURRENT FILING DATE: 2002-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                            LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 301-309-8439 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: HOOVEY, KEN1EY K.
REGISTRATION NUMBER: 40,302
REFERENCE DOCKET NUMBER: PF3
TELECOMMUNICATION INFORMATION:
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267 DSENSNFRNEIQSLV 281
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                                       1 DSEMYNFRSQLASVV 15
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TYPE: amino acid
STRANDEDNESS: single
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                                                                               Conservative
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53.3%;
                                                                                               56.2%; Score 41; DB 53.3%; Pred. No. 12;
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                                                                               Mismatches
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                                                                                                                        Length 281;
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CURRENT APPLICATION NUMBER: US/10/280,047
CURRENT FILING DATE: 2002-10-25

OF INVENTION: Human Tumor Necrosis Factor Receptor 10 REFERENCE: PF379P1D1

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RESULT 15
US-09-802-669-2
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Best Local Similarity
Wardhes 8; Conserve
                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-212-7
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US-09-826-212-7
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; ORGANISM: human
US-10-280-047-3
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PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/086,483
PRIOR PILLING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/069,112
PRIOR APPLICATION NUMBER: 60/069,112
PRIOR APPLICATION NUMBER: 60/050,936
PRIOR APPLICATION NUMBER: 60/050,936
PRIOR APPLICATION NUMBER: 60/144,023
PRIOR APPLICATION NUMBER: 60/144,023
PRIOR APPLICATION NUMBER: 60/142,563
PRIOR APPLICATION NUMBER: 60/142,563
PRIOR FILLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: 60/142,563
PRIOR FILLING DATE: 1999-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280006
CURRENT APPLICATION NUMBER: US/09/826,212
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
FEROMET 1.77
Sequence 2, Application US/09802669
PATENT NO. US20020004490A1
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Wei, Reiner
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                     Query Match 56.2%;
Best Local Similarity 53.3%;
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09826212 Patent No. US20010021516A1
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321 DSENSNFRNEIQSLV 335
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Search completed: November 26, 2003, 12:38:40 Job time : 27.1084 secs
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                                                                                                                                                    Matches
                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
FRIOR APPLICATION NUMBER: US 09/665,615
PRIOR PILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEG DATE: 1999-04-12
NUMBER OF SEG DATE: 1999-04-12
                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 15;
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Maximum DB seq
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
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                        AAW50173
AAW25604
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                                                                            Signal-transducing
Fas-antigen. Synt
PL peptide #12. S
CD95 PL peptide.
CD95 PL peptide.
C-terminal peptide
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                        C-terminal peptide
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     Human Fas.
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Drosophila melanog	ABB66326		193	54.8	40	
eripti	AAW33632		1066	•	41	4
TATA box binding p	AAR91300		1066	56.2	41	ū
Flk-lextraFAStm/cy	AAY97653		927	٠	41	2
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Human zinc metallo	ABU07731		805	٠,	41	5
	AAE20353	23	805	9	41	9
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angiote	AAY72667	22	805	٥,	41	4
Human MPROT15 amin	AAY67310	21	805		41	ũ
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human prote	AAU09092	22	711	٥.	41	7
Human TNFR1 protei	AAW64484	19	669	٥,	41	õ
Human expressed pr	ABU04642	24	436	٥,	41	9
CD44Hextra/tmFAScy	AAY97651	22	436	٥,	41	8
Apoptobody3sc fusi	AAY91026	21	436	٥,	41	?7
Human expressed pr	ABU04641	24	431	Ġ	41	9
CD44HextraFAStm/cy	AAY97650	22	431	9	41	Š
۳.	ABU07407	24	335	6	41	4
_	AABS0517	22	335	Ġ	41	23
(FAS	AAB01335	21	335	Ġ	41	22
Fas r	AAB36267	21	335	Ġ	41	21
o acid enc	AAB19341	21	335	ġ	41	õ
otei	AAW49104	19	335	ō	41	6
1 Fas	AAW50289	18	335	•	41	8
from	AAR92528	17	335	ō	41	7
Fas	AAR99681	17	335	ò	41	6
Fas protein	AAR78606	16	335	ò	41	5
cell	AAR28084	13	335	ō	41	[4
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e Fa	807	20	314	'n		ົວ
Fas solub	968	17	314	56.2	41	F
Fas-delta-TM. Hom	AAR76238	16	314	ġ	41	6

## ALIGNMENTS

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RESULT 1
AAW50173
ID AAW5
    Inhibition of signal transduction - by inhibiting binding between a signal-transducing protein and a cytoplasmic protein, for treating
                                  WPI; 1998-145347/13.
                                                         Sato T,
                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                               Inhibition; specific binding; signal-transducing protein; cytoplasmic protein; proliferation; cancer cell; apoptosis, virally infected cell.
                                                                                                                                                                                                                                                             Signal-transducing protein carboxy-terminal peptide
                                                                                                     22-JUL-1996;
                                                                                                                          18-JUL-1997;
                                                                                                                                                 12-FEB-1998
                                                                                                                                                                     WO9805347-A1.
                                                                                                                                                                                                                                                                                   16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                         AAW50173;
                                                                                                                                                                                                                                                                                                                             AAW50173 standard; peptide;
                                                                               (UYCO ) UNIV COLUMBIA NEW YORK.
                                                       Yanagisawa J;
                                                                                                     96US-0681219.
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viral infection

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                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                            The sequences given in AAW25604-05 are antigens which are used in the kits of the invention. The kits allow for immunological assay of Fas antigen. They comprise anti-Fas antibody specifically bound to an area of a cell showing Fas antigen, which is immobilised on an insoluble supporting material. The labelled anti-Fas antibody specifically binds to "out-of-area" of Fas antigen and standard Fas antigen extracted from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kit for immunological assay antibody specifically bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                              56.2%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Fas antigen - comprises anti-Fas to area of cell of Fas antigen
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Pred. No. 0.55
4; Mismatches
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Pred. No. 4.2e-07;
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                                                                                                                                                                                                                                                                  The present invention relates to a new method for modulating a biological function of an endothelial cell or hematopoistic cell. The method involves introducing into a cell, an antagonist that inhibits binding between a PDZ protein and a PL protein. The inhibitor is used to treat a disease mediated by hematopoietic cells, e.g. autoimmune disease. It may also be used to prevent transplantation rejection of a solid organ transplant. The method may also be used in the treatment of inflammation, allergy, inflammatory bowel diseases, ulcerative colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis, graft rejection, transplantation rejection), atherosclerosis, cancers, infectious diseases, ischemia, vasulitis and Crohn's disease.
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14-MAY-1999;
21-OCT-1999;
29-OCT-1999;
13-DEC-1999;
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                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating a biological function of an endothelial cell or hematopoietic cell, useful for treating autoimmune diseases and infectious diseases, by administerring an antagonist that inhibits binding between a PDZ protein and a PL protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allergy; asthma; multiple
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                                                                                                     8; Conserva
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DSENSNFRNEIQSLV
                                                 DSEMYNFRSQLASVV
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                                                                                                        Conservative
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; 2000US-0196460.
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99US-0160860.
99US-0162498.
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                                                                                                           4.
                                                                                                        Score 41; DB
Pred. No. 0.76
4; Mismatches
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                                                                                                           Indels
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                                                                                                              Gaps
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RESULT 4 AAB57663

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AAB57663 standard; Peptide; 20 AA.

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The present invention relates to a method for modulating a biological CC function of an endothelial cell or haematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a CC ppz domain protein and a PL domain protein to result in inhibition of leukocyte activation. The present sequence is a PL peptide. PDZ domains CC of proteins are named after three prototypical proteins: PSDS domains CC proteins are involved in synapse formation by organising transmembrane neurotransmitter receptors through intracellular interactions. The callibrations identified by the present invention can be used to treat a CC disease mediated by haematopoietic cells, e.g. autoimmune disease, clear asthma), atopic dermatitis, sutcimmune diseases (e.g. rheumatoid erratite, multiple sclerosis, insulin-dependent diabetes, Hashimoto CC thyroiditis, osteoarthritis), atherosclarosis, cancers, infectious CC disease (e.g. viral infection), ischaemia, vasulitis and Crohn's CC rejection of a solid organ transplant.
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14-MAY-1999; 99US-0134117.
14-MAY-1999; 99US-0160860.
29-OCT-1999; 99US-0160860.
29-OCT-1999; 99US-0170453.
13-DEC-1999; 99US-0170453.
14-JAN-2000; 2000US-0176195.
14-FEB-2000; 2000US-0182296.
11-APR-2000; 2000US-0196527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New inhibitors of binding of a PDZ protein and PL protein for inhibiting T cell-mediated response by hematopoietic cells, or treating diseases characterized by inflammatory and humoral ir responses, e.g. inflammation, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endothelial cell; haematopoietic cell; PDZ domain protein; PL domain protein; leukocyte activation; synapse formation; transmembrane neurotransitter autoimmune disease; transplantation rejection; inflammation; allergy; inflammatory bowel disease; ulcerative colitis; ileitis; pso asthma; atopic dermatitis; atherosclerosis; cancer; infectio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 51; 139pp; English
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cer; infectious disease;
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Query Match
Best Local Similarity 53...
Matches 8; Conservative

56.2%;

Score 41; DB Pred. No. 0.76 4; Mismatches 41; DB 22 No. 0.76;

22;

Length 20;

Indels

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Sequence

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           The present invention relates to a method for modulating a biological CC function of an endothelial cell or haematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a CC introducing into a cell an antagonist that inhibits binding between a CC ppz domain protein and a PL domain protein to result in inhibition of leukocyte activation. The present sequence is a PL peptide. PDZ domains CC of proteins are named after three prototypical proteins: PDZ domains CC proteins are involved in synapse formation by organising transmembrane convocatasmitter receptors through intracellular interactions. The CC neurotransmitter receptors through intracellular interactions. The CC inhibitors identified by the present invention can be used to treat a CC disease mediated by theamatopoietic cells, e.g. autoimmune disease, conflammation, allergy (e.g. drug allergies), inflammatory bowel diseases, concers, asthmal, atopic dermatitis, sutoimmune diseases (e.g. rheumatoid arthritis, osteoarthritis, insulin-dependent diabetes, Hashimoto chipping asthmal, osteoarthritis), anterosciptosis, insulin-dependent diabetes, infectious
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14-MAY-1999;
21-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endothelial cell; haematopoietic cell; PDZ domain protein; PL domain protein; leukocyte activation; synapse formation; transmembrane neurotransmitter receptor; autoimmune disease; transplantation rejection; inflammation; allergy; inflammatory bowel disease; ulcerative colitis; ileitis; pso asthma; atopic dermatitis; atherosclerosis; cancer; infectio
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11-APR-2000;
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 infection),
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RESULT 6
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                                                                                                                                                                                                                              The invention relates to methods and reagents for determining the apparent affinity (Kd) of binding between a PDZ domain and a ligand. The invention also relates to methods and reagents for determining the Ki of an inhibitor of binding between a PDZ domain and a ligand, identifying an agent that enhances binding of a PDZ domain and a ligand, and determining the potency (K-enhancer) of binding between a PDZ domain and a ligand, by determining the ligand bound with an immobilised polypeptide comprising a PDZ domain and a non-PDZ domain on a surface. The modulator (preferably, an inhibitor) of interaction between PDZ and PL is useful for treating a disease characterised by leukocyte activation, e.g., an autoimmune disease that is characterised by inflammatory or humoral immune response, and for reducing inflammation in a subject. This sequence represents a c-terminal peptide of a PDZ-binding protein relating to the invention.
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assays for determining the affinity of binding between a PDZ domain and a ligand, and determining the Ki of an inhibitor of the binding, comprises using a polypeptide comprising a PDZ domain and a non-PDZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
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                                                            Local Similarity hes 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                            The present invention describes a method (M1) for modulating a biological CC function of an endothelial cell or haematopoietic cell. M1 comprises CC introducing into the cell, an agent that inhibits binding of a PDZ CC (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein) CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the biological function. Also described is a method (M2) for determining CC whether a test compound is an inhibitor of binding between a PDZ protein CC and a PL protein. M1 is used for modulating a biological function of an CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an CC inhibitor (I) is useful for treating a disease characterised by leukocyte activation, where the disease is characterised by an inflammatory or cCC inhibitor (I) is useful for treating a disease characterised by leukocyte cactivation, where the disease is characterised by an inflammatory or CCC inflammatory and humoral immune responses e.g., inflammating (ameliorating complementary and humoral immune responses e.g., inflammation, allergy, inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis, ilertire and enteritis.
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24-NOV-2000; 2000US-0721915.
24-NOV-2000; 2000US-0722069.
28-NOV-2000; 2000US-0724553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 64; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating the biological function of an endothelial cell or hematopoietic cell e.g., a T-cell or B-cell comprises introducing into the cell, an agent that inhibits binding of a PDZ protein and a PDZ
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psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic diseases such as asthma, allergic rhinitis, transplantation rejection (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,

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RESULT 8
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                                                                                                                   The sequence represents the tumour necrosis factor receptor Fas death domain (Fas DD). The invention relates to a novel solution comprising a tumour necrosis factor receptor 1 death domain. The solution is useful for identifying a potential inhibitor of TNFR-1 DD, for the design and selection of potent and selective inhibitors of TNF signalling pathways, and for generating a three-dimensional structure for an unknown molecule
                                                                                                                                                                                                                              Solution comprising tumor necrosis factor receptor 1 death domain, useful for identifying potential inhibitor of tumor necrosis factor
                                                                                      Sequence
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                                                                                                                                                                                                                                                                                       Sukite SF, Xu G,
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TELLIEZ J.
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DSENSNFRNEIQSLV 119
                    DSEMYNFRSQLASVV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor; TNFR-1; death domain; co-ordinate data.
                                                                                                                                                                                                English.
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Pred. No. 0.76;
4; Mismatches
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RESULT 10
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                                                                                                                                                                                                                                                                       receptor family. A novel human tumour necrosis factor receptor, designated TR9, has been isolated. The TR9 receptor is also known as Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for treating, preventing or diagnosing common variable immunodeficiency, X-linked agammaglobulinaemia, severe combined immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and asthma), HTV infection, epilepsy, cancer, cardiovascular diseases and other neurological diseases.
                AAR76238;
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid molecule encoding a human tumor necrosis factor receptor, known as TR9, useful for treating, preventing and diagnosing severe combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     common variable immunodeficiency; X-linked agammaglobūlinaemia; severe combined immunodeficiency; Wiskott-Aldrich syndrome; autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis; multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer; cardiovascular disease; neurological disease; protein coordinate data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; cardiant; antiasthmatic; antidiabetic; antialler antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic; neuroprotective; gene therapy; Death Domain Containing Receptor 6;
                                             AAR76238 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 220pp; English.
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14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-594575/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Fas; tumour necrosis factor; TR9 receptor; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                        267
                                                                                                                                                     Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gentz RL,
                                                                                                                                                                                  Similarity
8; Conserv
                                                                                                                      DSENSNERNEIQSLV 281
                                                                                                                                                   DSEMYNFRSQLASVV 15
                                                                                                                                                                                                                                               281 AA;
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0126019.
99US-0134220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu G,
                                             Protein;
                                                                                                                                                                                               53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fan
                                             314 AA
                                                                                                                                                                                  4.
                                                                                                                                                                                                Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ָי
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                  16;
                                                                                                                                                                                                               21;
                                                                                                                                                                                                               Length 281;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coordinate data.
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ARESULT 11
AAR99682
ID AAR99
XX AAR99
XC AAR99
XC AAR99
XX IO-OC
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                    Fas antigen; autoim angioimmunoblastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mkNA was obtd. from human lymphocytes and PCR was used to make CDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli DH5-alpha cells. insert sequence of pBluescript-Fas-delta-TM encoded the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Peptide
Protein
                                                                                                                                                                                                                                               Human Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ93879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
adoptive immunotherapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
06-NOV-1995
                                                                                                                                                                                                                                                                                               10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                          AAR99682 standard; Protein; 314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig.3-1 to 3-4; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-200120/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-1993;
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                                               Peptide
                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LXRB-) LXR BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSEMYNFRSQLASVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSENSNFRNEIQSLV 314
                                                                                                                                                                                                                                             soluble antigen Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kiefer MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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(first en
                                                                                                                                                                      autoimmune disease; systemic lupus erythematosus; lastic lymphadenopathy; AILD.
                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0152443.
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  1..16
/label= Sig_peptide
17..314
                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Sig_peptide
                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
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Pred.
                                                                                                                                                                                                                                               de11.
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 314;
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RESULT 12
AAW98070
ID AAW98
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                          A natural, soluble Fas antigen variant (AAR99682), designated Fas dell, and other Fas variants (AAR99683-85) are derived by alternative splicing of Fas gene transcripts. A cDNA clone (AAR194527) coding for the variant was obtd. from human peripheral blood mononuclear cells. The Fas dell variant lacks the transmembrane domain of insoluble Fas antigen (AAR99681). Recombinant dell variant, or fragments of it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells. Detection of increased levels of soluble forms of Fas antigen can be used to diagnose autoimmune diseases, esp. systemic lupus erythematosus and angioimmunoblastic lymphadenopathy.
Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive; graft versus host disease; autoimmune disease; psoriasis; rheumatoid arthritis; systemic lupus erythematosus; gene therapy.
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 114-16; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natural, soluble form of Fas antigen secreted by human cells result of alternative mRNA processing - used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
                                                 Soluble Fas
                                                                          21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT34527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-321796/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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                                                                                                  AAW98070;
                                                                                                                          AAW98070 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UABR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1995;
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                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UAB RES
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                            DSEMYNFRSQLASVV
                                                                                                                                                                                       DSENSNFRNEIQSLV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Mountz
                                                                                                                                                                                                                                                                                       314 AA;
                                                 receptor
                                                                                                                                                                                                                                      Conservative
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0371263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Mat_protein
/note= "soluble Fas
17..168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161..171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169..314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "the 5 C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Extracellular_domain
                                                                                                                          Protein;
                                                                                                                                                                                                                                                56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "preferred peptide from breakpoint region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fas antigen extracellular domain deleted in Fas dell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (claim 4,
                                                                                                                                                                                                               15
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                                                                                                                          314
                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                 Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou
                                                                                                                          A
                                                                                                                                                                                                                                       ed. No. 18;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide from breakpoint page 132)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide from breakpoint region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   del1 antigen"
                                                                                                                                                                                                                                                              BB
                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                             Length 314;
                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                       Gaps
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RESULT 13
AAB50893
ID AAB50
XX
AC AAB50
XX
AC 19-MA
XX
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                                                                                                                                                                                                                                                                                                                            provides a method for inhibiting a proinflammatory response in a cell mixture by administering an immunosuppressive agent which in hibits the proinflammatory activity of Fas ligand (Fasi). In some embodiments, an Pasi is coadministered with the immunosuppressive agent, and the cell mixture comprises neutrophil cells. The method can be practised in vitro, ex vivo or in vivo. Suitable immunosuppressive agents include antisense molecules that inhibit endogenous Fasi expression, soluble Fas receptors or variants, ribozymes that inhibit the endogenous expression of Fasi, drugs that inhibit Fasi signalling, agents that induce the endogenous expression of transforming growth factor (TGF)-beta, and polynucleotides coding for an immunosuppressive agent such as polynucleotides coding for an immunosuppressive agent such as that an undesired Fasi-mediated proinflammatory response, e.g.
                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                            Matches
            19-MAR-2001
                                        AAB50893;
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                         graft versus host disease, or an autoimmune disease such as systemic lupus erychematosus, rheumatoid arthritis and psoriasis. The invention also provides a method for identifying agents which modulate Fasi stimulation of a proinflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This present sequence is a soluble Fas receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 4B; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibition of proinflammatory responses - using an agent which modulates Fast stimulation, used for treating graft versus hos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-132243/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia.
                                                                  AABS0893 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-1998;
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                                                                                                                                       300
                                                                                                                                                              H
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                          8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nabel GJ;
                                                                                                                                    DSENSNFRNEIQSLV 314
                                                                                                                                                               DSEMYNFRSQLASVV 15
                                                                                                                                                                                                                                                314 AA;
                                                                                                                                                                                          Conservative
            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9708-0052829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by GAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Bignal peptide"
17..314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "N-glycosylated"
                                                                  Protein, 331 AA
                                                                                                                                                                                                      56.2%;
                                                                                                                                                                                          4
                                                                                                                                                                                                      Score 41;
Pred. No.
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                       18;
                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                    Length 314;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                versus host
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                                                                                                                                                                                         Gaps
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Fas antigen;

apoptosis; pF58; NGFR/TNFR family.

Human cell surface antigen

Homo sapiens

25-MAR-2003 12-MAR-1993

(updated) (first entry)

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RESULT 14
AAR28084
ID AAR28
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                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is given in a specification relating to an isolated nucleic acid encoding a human tumour necrosis factor receptor TR10. The TR10 polynucleotide, polypeptide, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of cancer, such as breast and ovarian cancer and leukaemia; autoimmune disorders such as multiple sclerosis, Crohn's disease and graft versus host disease; disease associated with increased apoptosis such as AIDS, Alzheimer's disease and Parkinson's disease; cardiovascular disorders such as limb ischaemia and congenital heart defects; inflammatory diseases e.g. allergy; wound healing; disorders associated with neovascularisation, e.g. diabetic retinopathy; infectious diseases such as viral, bacterial, fungal and parasitic infections; and neurological diseases such as amyotrophic lateral sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-1999;
07-JUL-1999;
15-JUL-1999;
                                                                                                                                              AAR28084;
                                                                                                                                                                               AAR28084 standard; Protein; 335 AA
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 212pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding a tumor necrosis factor receptor 10, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders, and diseases and disorders associated with apoptosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-025250/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vasotropic; antiallergic; antidiabetic; vulnerary; ophthalmological; antiviral; antibacterial; antifungal; antiparasitic; gene therapy; tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder; apoptosis; cardiovascular disorder; inflammatory disease; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; TR10 receptor; cytostatic; immunosuppressive; neuroprotective; antiinflammatory; anti-HIV; antiparkinsonian; nootropic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Ni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Fas receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection; neurological disease; Fas receptor; protein coordinate data
                                                                                                                                                                                                                                                                317 DSENSNFRNEIQSLV 331
                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserv
                                                                                                                                                                                                                                                                                             DSEMYNFRSQLASVV 15
                                                                                                                                                                                                                                                                                                                                                                                               331 AA;
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99US-0142563.
99US-0144023.
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Pred. No.
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RESULT 15
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XX T9-FE
XX Plasm
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Peptide
   plasmid pF58; human Fas cDNA; soluble membrane protein; antibody production; diseases; treatment; prevention.
                                          Human Fas protein.
                                                                                      AAR78606;
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                      The Fas antigen is implicated in apoptosis. A cDNA clone encoding the antigen was isolated (pF58) and the antino acid sequence of Fas was deduced from it. The mature protein has a calculated mol.wt. oi 36,000 and is a member of the NGFR/TNFR family of cell-surface membrane proteins. The inventors claim a protein comprising at least the extracellular domain of Fas antigen. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                             Claim 3;
                                                                                                                                                                                                                                                                                                                                                                               DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monoclonal antibodies that react with tumour cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-358914/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                 19-FEB-1996
                                                                                                           AAR78606 standard;
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                                                                                                                                                                                                        Similarity 8; Conserv
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                                                                                                                                                             DSENSNFRNEIQSLV 335
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/note= "putative"
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                                                                 entry)
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Pred. No. 19;
4; Mismatches 3
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Matches 8
                                                                                                      AAR78606 (human Fas protein) is encoded by the plasmid pF58 which contains hFas cDNA. The plasmid was used in the construction of ar expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of related diseases.
                                                                                    Sequence
                                                                                                                                                                                         Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                      Example 1; Pages 15-17; 51pp; Japanese.
                                                                                                                                                                                                                          N-PSDB; AAQ95297.
                                                                                                                                                                                                                                                                                                                       09-MAY-1995.
                                                                                                                                                                                                                                                                                                                                           JP07115988-A
                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                    WPI; 1995-202847/27.
                                                                                                                                                                                                                                                                                                  26-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                             26-OCT-1993;
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 321
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8; Conserv
DSENSNFRNEIQSLV 335
                     DSEMYNFRSQLASVV 15
                                                                                    335 AA;
                                          Conservative
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1..16
/label= sig_peptide
17..335
/label= mat_peptide
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Search completed: November 26, 2003, 12:30:27 Job time: 42:5663 secs

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1 salmonella
6 african swi
2 agaricus bi
1 paramecium
7 mycoplasma
9 buchnera ap
homo sapien
0 kluyveromyc
4 saccharomyc
4 sorrelia bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 homo sapien
7 saccharomyc
9 saccharomyc
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apple chlor
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clostridium
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sus scrofa
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escherichia
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Q62230 mus musculu	O19911 cyanidium c			P47520 mycoplasma				Q61414 mus musculu	P24438 human herpe	Q8yln2 anabaena sp	Q65228 african swi

## ALIGNMENTS

R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	RR	RRI RR	RESUITING AC DIT
SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).  SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).  MEDLINE=96238926; PubMed=86488105;  MEDLINE=96238926; PubMed=86488105;  Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;  Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;  Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;  Papoff G., Cascino I., Ruberti G.;  Papoff G., Lynch D.H., Ruberti G., Lynch D.H., Ruberti G.;  Papoff G., Lynch D.H., Ruberti G.;  Papoff G., Lynch D.H., Ruberti G., Lynch D.H., Ruberti G.;  Papoff G., Lynch D.H., Ruberti G., Lynch D.H., Ruberti G.;  Papoff G., Lynch D.H., Ruberti G., Lynch D.H., Ruberti G.;  Papoff G., Lynch D.H., Ruberti G., Lynch D.H., Ruberti G.;  Papoff G., Lynch D.H., Ruberti G., Lynch D.H., Ruber	MEDLINE-95181785; PubMed-7533181; Cascino I., Fiucci G., Papoff G., Ruberti G.; "Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced by alternative splicing."; J. Immunol. 154:2706-2713(1995). [4] SEQUENCE FROM N.A. (ISOFORM 5). TISSUE-Peripheral blood lymphocytes; Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.	FROM N.A. (ISOFORM 1), AND SEQUENCE OF 2 92268122; PubMed=1375228; Behrmann I., Falk W., Pawlita M., Maier M., Richards S., Dhein J., Trauth B.C., P.H.; P.H.; ation and molecular cloning of the APO-1 a member of the tumor necrosis factor/ne superfamily. Sequence identity with the Chem. 267:1079-10715(1992).	ISOFORM 1). bMed=1713127; Ishii A., Yonehara M., Mizushim ., Seto Y., Nagata S.; oded by the cDNA for human cell stoosis.";	RESULT 1  TINE6_HUMAN STANDARD; PRT; 335 AA.  I TINE6_HUMAN STANDARD; PRT; 335 AA.  PRT 01-MAY-1992 (Rel. 22, C1eated)  DT 01-MAY-1992 (Rel. 22, Last sequence update)  DT 01-MAY-1992 (Rel. 42, Last annotation update)  DT 15-SEP-2003 (Rel. 42, Last annotation update)  DE receptor (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)  DE (CD95).  GN HOMO sapiens (Human).  OC ENCASTO (Human).  DE (CD95) (Homo sapiens (Human).  CHARMAIDAIGA (STANDARD).  CHARMAIDAIGA (STANDARD).

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RA Strausherg R. D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Histeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McTley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J. M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length
Thuman and mouse cDNA sequences.",
The Collins of th
Pensati L., Costan
Natoli G., Nisini
                                                                                        VARIANT ALPS ALA-28.
MEDLINE=97463833; PubMed=9322534;
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La Grutta S., Correra A., Notarangelo L.
"Missense mutations in the Fas gene resu
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MEDLINE=95277838; PubMed=7538908;

Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed "RIP: a novel protein containing a death domain Fas/APO-1 (CD95) in yeast and causes cell death.
                                                                                                                                                                                                                                                                                                                           Straus S.E.;
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MEDLINE=97122332; PubMed=8967952;
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                           Costanzo A., Ianni I
Nisini R., Almerighi
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the Fas (APO-1/CD95)
                           Accapezzato D., Iorio R.,
Balsano C., Vajro P., Vegnente
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Straus S.E., Jaffe B.S., Puck J.M., Dale J.K., Elkon K.B., Roesen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W. Fischer R.E., Jackson C.M., Lin A.Y., Baeumler C., Siegert Marx A., Valshnaw A.K., Grodzicky T., Fleisher T.A., Lenard "The development of lymphomas in families with autoimmune lymphoproliferative syndrome with germline Fas mutations an defective lymphocyte apoptosis."; Blood 98:194-200 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg I "Somatic Fas mutations in non-Hodgkin's lymphoma: extranodal disease and autoimmunity.";
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Jackson C.E., Fischer R.E., Hsu A.P., And
Dale J.K., Fleisher T.A., Middelton L.A.,
Straus S.E., Puck J.M.;
"Autoimmune lymphoproliferative syndrome '"Autoimmune syndrome '"Autoimmune syndrome '"Autoimmune syndrome '"Autoimmune syndrome '"Autoimmune syndrome '"Autoimmune syndrome syndrome syndrome syndrome syndrome syndrome syndr
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Gastroenterology 113:1384-1389(1997).
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Exp. Hematol. 27:868-874(1999).
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patient with
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Am. J. Hum. Genet. 64:10
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                                                       both. The secreted isofor
- SUBUNT: Binds DAXX (By some control of the control of
                                                                                                                          FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted isoforms 2 to 6 block apoptosis (in vitro). SUBUNIT: Binds DAXX (By similarity). Binds RIPK1.

SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
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LYS-264; LYS-272; PHE-278 AND I
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ink B., Martin H.,
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* Sneller M.C.,
                                  isoforms=6;
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T145_YEAST
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Best Local Similarity 53.0
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Transcription initiation factor TFIID 145 kDa
factor 145 kDa) (TAFII-145) (TAFII-130).
TAF145 OR YGR274C OR G9374.
           EMBL; U14954; AAA79178.1; -.
EMBL; X84098; CAA58896.1; -.
EMBL; Z73059; CAA97304.1; -.
                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Every the European Bioinformatice Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                COMPLEX from Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 92:824-8228(1995).
-I- FUNCTION: TARS ARE COMPONENTS OF THE TRANSCRIPTION FACTOR IID (TPIID) COMPLEX THAT ARE ESSENTIAL FOR MEDIATING REGULATION OF RNA POLYMERASE TRANSCRIPTION.
-I- SUBJUNIT: TEILD IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND FUNDBER OF TBP-ASSOCIATED FACTORS (TAPS) WHOSE MW RANGE FROM NUMBER OF TBP-ASSOCIATED FACTORS (TAPS)
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 368-384; 528-554 AND 752-783, AND STRAIN-YPH252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97279232; PubMed-9133740;
Ruzzi M., Marconi A., Saliola M., Fabiani L., Montebove F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Yeast TAFIIS in a multisubunit transcription.";
Nature 371:523-527(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales;
NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                              Poon D., Bai Y., Campbell A.M., Bjorklund S., Kim Y.
Kornberg R.D., Well P.A.;
"Identification and characterization of a TFIID-like
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95396770; PubMed=7667272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of a 8 kb
                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear (Potential). SIMILARITY: TO 8.POMBE TAPII-111. SOME, TO AND TO DROSOPHILA TAPII-230.
850237;
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There are no restrictions
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RESULT 3
DBPA_YEAST
ID DBPA Y
ID DBPA Y
ID DBPA Y
ID O1-NOV
DT 01-NOV
DT 02-PEB
OX MCBI_T
RN (2)
RR PAULI
DR PINEL
DR INTER
DR PART
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DR PROSI
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Best Local S
Matches 8
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
28-FEB-2003 (Rel. 4
InterPro; IPRO01410; DEAD.
InterPro; IPRO01659; HeliCase_C.
InterPro; IPRO01659; HeliCase_C.
InterPro; IPRO01650; HeliCase_C.
Pfam; pF00270; DEAD; 1.
Pfam; pF00271; heliCase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00490; DEAD_ATP_HELICASE; 1.
ATP-binding; RNA-binding; Helicase; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T01270; -.

SGD; S0003506; TAP145.

GO; GO:00004402; F:histone acetyltransferase activity; IDA.

GO; GO:000014; P:GI-specific transcription in mitotic cell c.

InterPro; IPR001978; Znf CCHC.

Pfam; PF000098; Znf-CCHC; T.

SMART; SM00343; ZnF C2HC; 1.

Nuclear protein; Transcription regulation.

Nuclear protein; Transcription regulation.

SEQUENCE 1066 AA; 120695 MW; FAFIEEZA9B2A7B73 CRC64;
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Probable RNA-dependent helicase DBP10 (DEAD
DBP10 OR YDL031W OR D2770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burger F., Daugeron M.-C., Linder P.;
"Dbp10p, a putative RNA helicase from Saccharomyces cerevisi
"equired for ribosome biogenesis.";
required for ribosome biogenesis.";
Nucleic Acids Res. 28:2315-2323 (2000).
-!- FUNCTION: PUTATIVE ATP-DEPENDENT RNA HELICASE. PROBABLY
WITH 60S RIBOSOMAL SUBUNIT. INVOLVED IN THE MATURATION C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetina;
Saccharomycetales; Saccharomycetaceae; Saccharon
NCBI_TaxID=4932;
                                                                                                                                                                                                                       EMBL; Z71781; CAA96458.1; -.
EMBL; Z74079; CAA98590.1; -.
PIR; S67564, S67564.
HSSP; Q58083; 1HV8.
                                                                                                                                                                                                                                                                                                                         modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
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Paulin L., Saren A.M.
Submitted (APR-1996)
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S0002189; DBP10.
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SITE
SEQUENCE
          Enterobacteriaceae;
                                           Hypothetical transcriptional YAGI OR B0272.
                                                                    01-NOV-1997
16-OCT-2001
                                                                                         P77300;
01-NOV-1997
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                           EMBL; U27121; AAA96952.1; -
ZFIN; ZDB-GENE-990415-81; 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P47805;
01-FEB-1996
                     Bacteria; Proteobacteria; Gammaproteobacteria;
                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mech. Dev. 52:383-391(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              differential RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A novel gene expressed during zebrafish gastrulation identified
                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for comparing the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: Gastrulation specific. SIMILARITY: BELONGS TO THE SPOT14 FAMILY.
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LOPMENTAL STAGE: Gastrulation
                                                                                                                                                                                              DSEMYNFRSQLASV 14
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288
995
                                                                                                                                                                                                                                                                  152
                                                                (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8541223;
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291
113157
                                                                                                                                                                                                                                                                 15-81; g12.
17486 MW;
           Escherichia
                                                                                                                                                                                                                              52.1%;
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                                                                                                                                                                                                                    Score 38; DB
Pred. No. 4.2;
6; Mismatches
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Pred. No.
                                                       regulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Danio rerio)
                                                                                                                                                                                                                                                                  140BE173FFC8E0A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 AA
                                                                                                                 252
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                                                       yagI
                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                         Length 152;
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                      Enterobacteriales;
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Best Local S
Matches '7
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SN HUMAN STANDARD; PRT; 1709 AA.
Q9BZZ2; Q96DL4; Q9GZS5; Q99H1H6; Q9H1H7; Q9H7L7;
16-OCT-2001 (Rel. 40, Created)
15-SEP-2003 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00346; HTH_ICLR; 1.
PROSITE; PS01051; HTH_ICLR_FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EcoGene; Edi3349; yagI.
EcoGene; Edi3349; yagI.
InterPro; IPR005471; HTH_IclRlike
InterPro; IPR005473; HTH_IclRlike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                          TISSUE=Monocytes;
MEDLINE=20575418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
DNA_BIND 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01614; IclR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000135;
EMBL; U70214; AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schramm S., Duncan M., Allen E., Ara
Davis K., Federspiel N., Hyman R., F
Lashkari D., Lew H., Lin D., Namath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Science 277:1453-1474(1997).
                                               Crocker P.R.;
                                                                      Hartnell A., Steel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; H64752; H64752
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                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                      'Characterization of
                                                                                                                                                                                                                                                                                                                  (CD169 antigen).
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expressed
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                                                                                            PubMed=11133773;
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                                                                                                                                               (ISOFORM 1),
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27838 MW;
                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.1%;
                         human sialoadhesin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Allen E., Alo
  resident
                                                                        Turley H.,
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Pred. No. 7.5;
2; Mismatches
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     and inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli K-12.";
                                                                        Jones M.,
                                                                                                                                                 CHARACTERIZATION
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7.5;
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                           a sialic acid binding
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                                                                           Jackson D.G.
                                                                                                                                                                                                                                                                                                                                           Ig-like lectin-1) (Siglec-
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  macrophage
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populations."; Blood 97:288-296(2001).

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RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RM ADLINE-21638749; PubMedel11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,

RA Deloukas P., Matthews L.H., Ashurst J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Basley J., Barlow K.F., Bates K.N., Carder C., Carter N.P.,

RA Basley J., Barlow K.F., Collier R.E., Connor R.E., Corby N.R.,

Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Collson A., Coville G.J., Praser A., French L., Garner P.,

RA Collson A., Coville G.J., Praser A., French L., Garner P.,

RA Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Johnson D.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Phillimore B.J.C.T., Patell R., Pearce T.A.V., Peck A.I.,

RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Tracey A., Tromans A.C., Vaudin M., Walli M., Wallis J.M.,

RA Wilhing L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Hillims S.A.,
                                                                                                                                                                                                                                                                                                                                               Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y., Matsumwa Y., Moriya S., Chiba E., Momiyama H., Onogawa S., Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R., Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y., Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Watanabe M., Sugiyama T., Isanamoto J., Isono Y., Kawai-Hio Y., Saito Mishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Sekine M., Kikuchi H., Kanda K., Maguho Y., Nagai K., Isogai T., Nasano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Nasano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Nasano S., Nagahari K., Masuho Y., Nagai K., Isogai T.
                                                                                                                                                                        Rogers J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21082933; PubMed=11214971;
Hattori A., Okumura K., Nagase T.,
"Characterization of long cDNA clor
DNA Res. 7:357-366(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The DNA sequence and comparative Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1539-1709 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF
                                                                                                                          Event-Alternative sp
Comment-Additional
                                                                                                                                                             ALTERNATIVE PRODUCTS:
 IsoId=Q9BZZ2-3; Sequence=VSP_002572;
Note=No experimental confirmation available;
                                                      IsoId=Q9BZZ2-2;
                                                                                         IsoId=Q9BZZ2-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              733-1709
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                                                                                                                          splicing; Named isoforms=3;
nal isoforms seem to exist;
                                                   Sequence=VSP_002571
                                                                                       Sequence=Displayed;
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man adult spleen.
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K., Isogai T.,
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, Ota T.,
v., Saito )
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IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 3
IG-LIKE C2-TYP

POTENTIAL. CYTOPLASMIC

(POTENTIAL)

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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Expressed by macrophages in various tissues. High levels are found in spleen, lymph node, perivascular macrophages in brain and lower levels in bone marrow, liver Kupffer cells and lamina propria of colon and lung. Also expressed by inflammatory macrophages in rheumatoid arthritis.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (STALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 immunoglobulin-like V-type domain SIMILARITY: Contains 16 immunoglobulin-like C2-type doma.
                                                                                                                                                                                                                                                DATABASE: NAME=PROW; NOTE=PROW 2:18-22(2001); WMW="http://www.ncbi.nlm.nih.gov/prow/guide/985165905_g.htm".
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EMBL; AF230073; AAK00757.1; -.
EMBL; AL109804; CAC17543.1; -.
EMBL; AL109804; CAC17542.1; -.
EMBL; AK024462; BAB15752.1; -.
EMBL; AK024452; BAB15749.1; -.
EMBL; AK024479; BAB15769.1; -.
EMBL; AK024479; BAB15769.1; -. PROSITE; PS50835; IG\_LIKE; 14. Cell adhesion; Lectin, Arri-MIM; 600/51; -...

GO; GO:0016021; C:integral to membrane; NAS

GO; GO:0005530; F:lectin; NAS.

GO; GO:0007160; P:cell-actix adhesion; NAS.

GO; GO:0007160; P:cell-actix adhesion; NAS.

GO; GO:0006954; P:inflammatory response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig\_c2. InterPro; IPR003006; Ig\_MHC. SM00408; IG HGNC:11127; Lectin; domain; 1709 1662 17662 17662 1366 136 320 402 402 507 507 507 507 507 507 1083 11165 8944 8944 11348 11442 11528 SN. Antigen; Transmembrane; Signal; Glycoprote Repeat; Alternative splicing; Polymorphism BY SIMILARITY.
SIALOADHESIN.
EXTRACELLULAR (POTENTIAL) response; NAS Glycoprotein;

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collaboration -

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AC P123

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SEQUENCE OF 392-759 FROM N.A. MEDLINE=94179260; PubMed=7510693; Lubin I.M., Healey J.F., Scandell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FA8 PIG STANDARD; PRT; 2133 AA. P12563, Q95243; Created) 01-OCT-1989 (Rel. 12, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Coagulation factor VIII precursor (Procoagulant F8 OR CF8.
                                                                                                                                                                                                                                            SEQUENCE OF 705-1573 FROM N.A. MEDLINE=86287369; PubMed=3016730; Toole J.J., Pittman D.D., Orr E.C.,
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Healey J.F., Lubin I.
Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                           Kaufman R.J., I
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                                                                                                                               large region (approximately equal to 95 kDa) of human factor VIII dispensable for in vitro procoagulant activity."; oc. Natl. Acad. Sci. U.S.A. 83:5939-5942(1986).
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to the EMBL/GenBank/DDBJ
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                            Scandella
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N-LINK
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                         Runge M.S., Lollar P.;
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                                                                                                                                                                                                                                                                                                                                                                databases
                                                                                                                                                                                                                                                  Wasley L.C.,
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                               InterPro; IPRO01117; Cu-oxidase.
InterPro; IPR000421; FA58_C.
Pfam; PF00794; Cu-oxidase; 3.
Pfam; PF00794; F5_F8_type_C; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00231; FA58C; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS01286; FA58C_3; 2.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
Blood coagulation; Repeat; Plasma; Acute p
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-!- FUNCTION: FACTOR VIII, ALONG WITH
AS A COFACTOR FOR FACTOR IXA WHEN
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PIR; A25945; A25945.
PIR; T42763; T42763.
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-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: Contains 3 F5/8 type A domains.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: STRONG, TO COAGULATION FACTOR V.
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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davles R.M., Feltwell T., Holroyd :
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
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                                                                                                                                                                                      SEQUENCE :
                                                                                                                                                                                                                                              EMBL; AL139076; CAB72979.1; PIR; D81341; D81341. InterPro; IPR002678; DUF34. Pfam; PF01784; NIF3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne reveals hypervariable sequences.";
Nature 403:665-668(2000)
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Syntaxin 8 (SNARE protein related interacting protein 2).
SYN8 OR UIP2 OR YAL014C OR FUN34.
EMBL; AY205237; AA046883.1; -. EMBL; AY205236; AA022142.1; -. EMBL; L05146; AAC04943.2; -.
                                                                                       between the Swiss Institute of Bloinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequencing of chromosome of a 32 kb region between Genome 36:32-42(1993).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dolinski K.J., Cherry J.M.;
Submitted (DEC-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barton A.B., Kaback D.B.;
"Molecular cloning of chromosome I DNA from Saccharomyces analysis of the genes in the FUN38-MAK16-SPO7 region.";
J. Bacteriol. 176:1872-1880(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288c / AB972;
MEDLINE=94193531; PubMed=8144453;
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Ouellette B.F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burri L., Hofmann K., Lithgow T.;
"Re-sequencing of the UIP2 gene reveals a frame-correction
OC-SNARE in the endosome of Saccharomyces cerevisiae.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
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15-SEP-2003 (Rel.
Syntaxin 8 (SNARE
                                                                                                                                                                                                                                                                     proteins.
SUBCELLULAR LOCATION: Type IV membrane protein; endosome.
SIMILARITY: BELONGS TO THE SYNTAXIN/EPIMORPHIN FAMILY.
SIMILARITY: Contains 1 t-SNARE coiled-coil homology.domain.
                                                                                                                                                                                                                                                                                                                                                                                                         nitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. FUNCTION: t-SNARE which may play a role in determining specificity of membrane fusion, protein transport and trafficking within the Golgi/endosomal and plasma
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e B.F.F., Clark M.W., Keng T., Storms R.K., Zhong W.W.,
Fortin N., Delaney S., Barton A.B., Kaback D.B., Bussey H.;
ing of chromosome I from Saccharomyces cerevisiae: analysis
kb region between the LTE1 and SPO7 genes.";
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Bussey H.,
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SGD; S0000012; YAL014C.

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RESULT 10
YN33_YEAST
ID YN33_Y
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28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 73.0 kDa protein in CLA4-PUS4 intergenic region.
                                                                                               SEQUENCE
                                                                                                                                       SMART; SM00164; TBC; 1.

PROSITE; PS50086; TBC RABGAP; 1.

Hypothetical protein; Transmembrane.

TRANSMEM 329 349 POTENTIAL.

TRANSMEM 422 442 POTENTIAL.
                                                                                                                                                                                                                                                     GO; GO:0005934; C:bud tip; IDA.
GO; GO:0000131; C:incipient bud site; I
GO; GO:0005097; F:RAB GTPASE activator
InterPro; IPR000195; RabGAP_TBC.
Pfam; PF00566; TBC; 1
                                                                                                                                                                                                                                                                                                                                                                       PIR; S60408; S60408.
SGD; S0005237; MSB3.
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U23084; AAC49106.1; -. EMBL; Z71569; CAA96211.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Su or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel putative serine/threonine protein kinase
Yeast 11:1303-1310(1995).
-!- SIMILARITY: Contains 1 Rab-GAP TBC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96132033; PubMed=8553702;
Maurer K.C.T., Urbanus J.H.M., Planta R.J.;

"Sequence analysis of a 30 kb DNA segment from yeast chromosome carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=S288c /
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P48566;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                    DOMAIN
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  Similarity 7; Conserv
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••
  Score 37; DB Pred. No. 33; 2; Mismatches
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T-SNARE COILED-COIL HOMOLOGY.
; 7631FB672F8E55D6 CRC64;
                                                                                            RAB-GAP TBC.
; 5F62607B95BBAFB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
ANCHOR FOR TYPE IV MEMBRANE PROTEIN
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12;
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RESULT 11
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SEQUENCE
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Q91713;
Q91-NOV-1997
                                                                                                                    DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                              SMART; SMUVGLT; WFC_1; 2.
PROSITE; PS01208; VWFC_2; 3.
PROSITE; PS50184; VWFC_2; 3.
                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Xenopus chordin: a novel dorsalizing factor activated by organize specific homeobox genes.";

Cell 79:779-790(1994).

-i- FUNCTION: POTENT DORSALIZING FACTOR. HAS POTENT AXIS-FORMING ACTIVITIES INCLUDING THE ABILITY TO RECRUIT NEIGHBORING CELLS ACCIVITIES INCLUDING THE ABILITY TO RECRUIT NEIGHBORING CELLS
                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                        SMART; SM00566; SOG; 3.
SMART; SM00214; VWC; 4.
                                                                                                                                                                                                                                                                                                        EMBL; L35764; AAC42222.1; -. PIR; A55195; A55195.
                                                                                                                                                                                                                                                                                                                                                or send an
                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de Robertis E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Dorsal lip
MEDLINE=95094250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Last annotation update)
Chordin precursor (Organizer-specific secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                   Pfam; PF00093; vwc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             InterPro; IPR006559; SOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (enopodinae;
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TISSUE SPECIFICITY: PRECORDAL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 4 VWFC domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: EMBRYOGENESIS. SIMILARITY: BELONGS TO THE CHORDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HINGE; EXPRESSION CLOSELY FOLLOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CENTERS OF HEAD, TRUNK AND TAIL DEVELOPMENT.
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  Similarity 7; Conserv
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                                                                                                                     at; Glycoprotein; S
POTENTIAL.
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VWFC 1.
VWFC 2.
VWFC 2.
VWFC 3.
VWFC 4.
Pred. No. 52;
3; Mismatches
                                                                                N-LINKED
                         Score 37;
                                                                   N-LINKED
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Best Local 9
Matches 7
                                                                                                                                                                                                                         R_SALTY
SPAR_SAI
P40701;
                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Surface presentation of antigens protein sp
SPAR OR STM2888
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Pituitary;

MEDLINE-96199202; PubMed=8621616;

Lester L.B., Coghlan V.M., Nauert B., Scott J.D.;

"Cloning and characterization of a novel A-kinase anch

AKAP 220, association with testicular peroxisomes.";

J. Biol. Chem. 271:9460-9465(1996).

-I- FUNCTION: BINDS TO TYPE II REGULATORY SUBUNITS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
A-kinase anchor protein 11 (Protein kinase A anchoring protein 11)
(PRKA11) (A kinase anchor protein 220 kDa) (AKAP 220).
                                                                   Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                  Enterobacteriaceae;
                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND ANCHORS/TARGETS THEM.
SUBCELLULAR LOCATION: ASSOCIATED WITH PEROXISOME.
TISSUE SPECIFICITY: Expressed in brain and testis.
DOMAIN: RII-ALPHA BINDING SITE, PREDICTED TO FORM AN AMPHHELIX, COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS
COMPLEMENTARY SURFACE ON THE R-SUBUNIT DIMER.
                                                                                                                                                                                                                                                      SALTY
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7; Conser
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14
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                                                                                                                                                                                                                                                      STANDARD;
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                     Salmonella.
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                   ation update)
protein spaR
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Best Local S
Matches · 8
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Q00946;
Q1-APR-1993
Q1-APR-1993
28-FEB-2003
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TRANSMEM
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InterPro; IPR002010; Bac export 1.
InterPro; IPR002010; Bac export 1.
InterPro; IPR002010; SpaR yscT.
Pfam; PF01311; Bac export 1; 1.
PRINTS; PR00953; TYPB3IMERROT.
         Viruses; dsDNA vi
NCBI_TaxID=10498;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:852-856 (2001).

-i- FUNCTION: INVOLVED IN A SECRETORY PATHWAY RESPONSIBLE FOR SURFACE PRESENTATION OF DETERMINANTS NEEDED FOR THE ENTRY SALMONELLA SPECIES INTO MAMMALIAN CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latre Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., L. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvan Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Groisman B.A., Ochman H.;
"Cognate gene clusters govern invasion of host epithelial cells Salmonella typhimurium and Shigella flexneri.";
EMBO J. 12:3779-3787(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
MEDLINE=94008985; PubMed=8404849;
                                    African swine fever virus (strain BA71V) (ASFV)
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE008832; AAL2 PIR; S37309; S37309.
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MEDLINE=21534948; PubMed=11677609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.

    -1- SUBCELLULAR LOCATION: Integral membrane protein ()
    -1- SIMILARITY: BELONGS TO THE FLIR/MOPE/SPAR FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               Virulence; Transmembrane;
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Ms; TIGR01401; flir
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                       dsDNA viruses,
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182
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25, Last sequence up
41, Last annotation
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Pred. No.
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POTENTIAL.
POTENTIAL.
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                       stage;
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                                                            n update)
3.4.22.-).
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                         Asfarviridae; Asfivirus.
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19;
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S., Laymar
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Best Local S
Matches 6
SEQUENCE FROM N.A.
STRAIN-ATCC 24666 / AG4;
MEDLINE=91347410; PubMed=1879001;
Robison M.M., Royer J.C., Horgen P.A.;
"Homology between mitochondrial DNA of Agaricus bisporus and
                                                                                                                                Eukaryota; Fungi; Basidio
Agaricales; Agaricaceae;
NCBI_TaxID=5343;
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MUTAGEN
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                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable DNA polymerase (EC 2.7.7.7) (Fragment).
Agaricus bitorquis (Pavement mushroom).
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01-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMO-1-specific protease family."; J. Biol. Chem. 276:780-787(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanez R.J., Rodriguez J.M., Nogal M.L., Rodriguez J.F., Vinuela E.; "Analysis of the complete nucleotide se
                                                                                                                                                                                                                                  Mitochondrion.
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PIR; A42549; A42549.
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SUBCELLULAR LOCATION: C
SIMILARITY: Belongs to
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187
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168
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Belongs to peptidase family C48.
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C->S: LOSS
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Job time

Search completed: November 26,

2003,

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Best Local S
Matches 7
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Interpro; IPR006172; DNA_pol_B.

Interpro; IPR004868; DNA_pol_B 2.

Pfam; PF03175; DNA_pol_B 2; T.

SMART; SM00486; POIBC; T.

SMART; SM00486; POIBC; T.

PROSITE; PS00116; DNA_POLYMERASE B; FALSE NEG.

Transferase; DNA-directed DNA polymerase; DNA re
DNA-binding; Plasmid; Mitochondrion.

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SEQUENCE 797 AA; 91922 MW; 5C49EAF51FB7F927
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                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 use
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type I site-specif	hypothetical prote	probable aminotran	hypothetical prote	sulfate adenylyltr	hypothetical prote	probable peptide A	hypothetical prote	hypothetical prote	cytoplasmic dynein	probable DNA-direc		hypothetical prote	hypothetical prote	beta-fructofuranos	nifS protein homol

## ALIGNMENTS

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RESULT 2
T49486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical conserved protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38520 C;Accession: T38520 R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
                                                                                          A; Map position: 6
C; Superfamily: Neurospora
                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-199 <SCH>
A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.380
A;Experimental source: BAC clone B14D6; strain OR74A
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A; Accession: T49486
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A; Introns: 74/2; 203/2
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A;Residues: 1-216 <OLI>
A;Residues: 1-216 <OLI>
A;Cross-references: EMBL:Z99259; PIDN:CAB16369.1; GSPDB:GN00066; SPDB:SPAC2C4.09
A;Experimental source: strain 972h-; cosmid c2C4
                                                                                                                                        A; Gene: NCSP: B14D6.380
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A;Gene: SPDB:SPAC2C4.09
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A; Accession: T38520
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Conservative
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                       57.5%;
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2; Mismatches
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                       Score 42; I
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A;Molecule type: nucleic acid
A;Residues: 1-134, Q',135-335 <OEH>
A;Residues: 1-134, Q',135-335 <OEH>
A;Residues: 1-134, G',135-335 <OEH>
A;Residues: 1-134, G',135-335 <OEH>
A;Rote: sequence extracted from NCBI backbone (NCBIP:103810)
A;Note: in NCBI backbone the source is designated as mouse
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                                                                            A; Map position:
                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X63717; NID:g28741; PID:g28742
R;Ochm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rich J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member A;Reference number: A38142; MUID:92268122; PMID:1375228
A;Accession: A38142
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                                                                                                A; Cross-references: GDB:132671; OMIM:134637
                                                                                                                            A;Gene: GDB:APT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: surface antigen APO-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Cascino, I.; Flucci, G.; Papoff, G.; Ruberti, J. Immunol. 154, 2706-2713, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-335 <KRJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: S24543
A;Accession: S24543
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A; Title: Three functional
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;Map position: 10q24.1-10q24.1
;Superfamily: NGF receptor repeat homology
;Reywords: apoptosis; surface antigen; transmembrane
;1-16/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ell 66, 233-243, 1991
;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can medi
;Reference number: A40036; MUID:91309137; PMID:1713127
;Accession: A40036
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;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
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A;Molecule type: DNA
A;Residues: 1-1066 <REES
A;Cross-references: EMBL:U14954; NID:g595837; PID:g595838
R;Reese, J.C.; Apone, L.; Walker, S.S.; Griffin, L.A.; Green, M
Nature 371, 523-527, 1994
A;Title: Yeast TAR(II)s in a multisubunit complex required for .
A;Reference number: 862389; MUID:95021683; PMID:7935765
A;Recession: S62389
A;Status: nucleic acid sequence not shown
                                                                     R;Poon, D.; Bai, Y.; Campbell, A.M.; Bjorklund, S.; Kim, Proc. Natl. Acad. Sci. U.S.A. 92, 8224-8228, 1995
A;Title: Identification and characterization of a TFIID-A;Reference number: S62390; MUID:95396770; PMID:7667272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATA box-binding protein-associated factor chain TAFII145 - yeast (Saccharon N, Alternate names: protein G9374; protein YGR274c; TAFII130 protein C;Species: Saccharones cervisiae C;Date: 27-Jan-1995 #sequence revision 10-Feb-1995 #text change 21-Jul-2000 C;Accession: S50237; S62389; S62397; S62394; S62395; S64607 C;Accession: S50237; S62389; S62397; S62394; S62395; S64607 R;Reese, J.C.; Apone, L.; Walker, S.S.; Griffin, L.A.; Green, M.R.
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A;Residues: 1-804 <WAM>
A;Cross references: EMBL;AL110224
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C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14762
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A;Accession: 862397
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A; Residues: 1-1066 < REW >
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A;Accession: S50237
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                                                 A; Accession: S62394
                                                                                                                                                                A; Residues: 583-599; 651-671 < REF >
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A; Accession: T14762
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                                                                                                                                                                                              A; Molecule type: protein
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Molecule type: DNA
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PMID:7667272
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R.D.,

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A;MOLECULE type: protein
A;Residues: 368-384;528-554;752-783 <POW>
R;Panzeri, L.; Agostoni Carbone, M.L.; Melcl
submitted to the Protein Sequence Database,
A;Reference number: S64591
                                                                                                                                                         potassium transport protein KUP1, high-affinity - Arabidopsis thaliana N;Alternate names; protein T27E13.19 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Mar-1999 #sequence revision 05-Mar-1999 #text_change 23-Mar-C;Accession: T00591; T02479; B84704 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, May 1998 A;Description: Arabidopsis thaliana chromosome II BAC T27E13 genomic se A;Reference number: Z14178
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                                                                      A/Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-712 <ROU>
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A;Residues: 1-1066 <PAN>
A;Cross-references: EMBL:273059; NID:g1323498; PID:e243586; PID:g1323499; MIPS:YGR274c
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A: Residues: 1-356 < KUR>
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C<sub>/</sub>Species: Sulfolobus solfataricus
                                                                                                                                             A,Accession: T00591
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A;Accession: D90313
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Jescription: Sulfolobus solfataricus complete genome
;Cross-references: EMBL:ACO04165; NID:g3150396; PID:g3150413;Experimental source: cultivar Columbia
;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S64607
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57.1%;
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Pred. No.
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Pred. No.
                                                                                                                                                                                    chromosome II BAC T27E13 genomic sequence
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base, May 1996
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M.L.; Brandon,
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R.C.;
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                   C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 (;Accession: F71719  
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998  
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893  
A;Accession: F71719
                                                                                                                                                                                    hypothetical protein RP104 - Rickettsia prowazekii C;Species: Rickettsia prowazekii
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  A;Status: preliminary; nucleic
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RESULT 9
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A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: F97717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AC004680; NID:g3420043; PID:g3420045
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                A;Residues: 1-993 <KUR>
A;Cross-references: GB:AE006914;
                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-993 < KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 15/3; 97/1; 179/1; 196/1; 283/1; 300/3; 339/1; C; Superfamily: barley probable potassium transport protein
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A; Residues: 1-712 <STO>
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A; Accession: B84704
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A; Residues: 1-712 < ROW >
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                                                                                                                                                                            A;Gene: RC0142
                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical
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                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /pothetical protein RC0142 [imported] - Rickettsia conorii (strain Malish
,Species: Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
                                                                                         Matches
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8; Conserv
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MYNESSQLA 724
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53.8%;
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Pred. No.
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Pred. No. 33;
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; Mismatches
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acid sequence not shown; translation

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A;Cross-references: SGD:S0002189
A;Map position: 4L
C;Keywords: ATP; nucleotide binding; P-loop
F;181-188/Region: nucleotide-binding motif A
F;284-289/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A;Title: Comparative genomics of Listeria species, A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1084
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C;Accession: AH1084
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; An
                                                                                                                                                                                                                                                                                                           R; Paulin, L.; Saren, A.M.; Laamanen, submitted to the Protein Sequence Da
                                                                                                                                                                                                                                                                                                                                                                 C;Species: Saccharomyces cerevisiae C;Date: 12-Jul-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YDL031w - yeast (Saccharomyces N;Alternate names: hypothetical protein D2770
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A;Experimental source: strain S288C
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A; Residues: 1-995 < PAU>
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A;Experimental source: strain EGD-e
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58.3%;
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88.9%;
 53.4%;
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Dussurget, O.; Entian,
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.A.; Voss, H.; W
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tian, K.D.; |
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Fsihi, H.
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probable transcription regulator yagI - Escherichia coli (strain K-12) C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 C;Accession: H64752 C;Accession: H64752 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F.A.; Rose, D.J.; Mau, B:; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-1030 <ZUM>
A;Residues: 1-1030 <ZUM>
A;Cross-references: EMBL:X83121; NID:g600461; PIDN:CAA58190.1;
A;Cumstein, E.; Pearson, B.M.; Kallgeropoulos, A.; Schweizer, N.
Submitted to the Protein Sequence Database, July 1996
A;Gene: yagI
C;Superfamily: acetate operon repressor
C;Keywords: DNA binding; transcription
F;186-207/Region: helix-turn-helix moti
                                                                                                                     A;Cross-references: GB:AE000135; GB:U00096; NID:g1786465; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                        Science 277, 1453-1462, 1997
A,Title: The complete genome
A,Reference number: A64720; M
A,Accession: H64752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: transmembrane protein F;131-171/Domain: GAL4 zinc binuclear cluster homology <GAL4>
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A;Map position: 15L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: Ī-1030 <ZUW>
A;Cross-references: EMBL:Z74831; NID:g1419931;
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast 11, 975-986, 1995
A;Title: A 29.425 kb segment
A;Reference number: S57374; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_chan c;Accession: S57380; S66783; S50416 R;Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, Yeast 11, 975-986, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein YOL089c - yeast (Sa.
N;Alternate names: hypothetical protein C0938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Saccharomyces cerevisiae
                                                                                                                                                                    A;Residues: 1-252 <BLAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: SGD: HAL9
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Best Local :
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MUID:97426617; PMID:9278503
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Pred. No. 53;
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                                                                                                                                                                                                                    sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                Bloch, C.A.; Perna, N.T.; Burland, V.; Riley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yeast (Saccharomyces cerevisiae)
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                                                                                                                                              PIDN:AAC73375.1; PID:g1786468
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hypothetical protein F35C8.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16257
Search completed: November 26, 2003, 12:36:07 Job time: 14.9157 secs
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                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: CES9:F35C8.8
A;Introns: 18/3; 40/2; 72/2; 113/2; 236/1; 269/1
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T16257
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                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-312 <WUX>
A;Cross-references: EMBL:U40941; NID:g1072184; PID:g1072190; PIDN:AAA81712.1; CESP:F35C8
                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F35C8.
A;Reference number: Z18486
A;Accession: T16257
                                                                                                                                                                              Query Match 52.1%; Score 38; DB 2; Length 312; Best Local Similarity 53.8%; Pred. No. 21; Matches 7; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.1%; Score 38; DB 2; Length 252; Best Local Similarity 63.6%; Pred. No. 16; Matches 7; Conservative 2; Mismatches 2; Indels
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227 DAELANFREQL 237
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39 EMHNFLNQLLQIV 51
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                 Score
      SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_funer:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_bage:*
10: sp_bage:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate
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Match
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73
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     1 DSEMYNFRSQLASVV 15
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_vertebrate:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archane.*
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804
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193
356
712
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1124
 Q81UB7
Q81UB6
Q9UFZ6
Q9BYF1
Q9MSS5
Q97Y08
022397
050043
052244
Q8EGQ4
Q8EGQ4
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Ol4042 schizosacch
Q8iub6 homo sapien
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Q9ufz6 homo sapien
Q9ufz6 homo sapien
Q9ufz7 homo sapien
Q9ufz7 homo sapien
Q9ufz8 drosophila
Q97y08 sulfolobus
Q22397 arabidopsis
Q52397 arabidopsis
Q52365 rickettsia
Q9265 rickettsia
Q9ze44 rickettsia
Q8ze40 shewanella
Q8ezd0 leptospira
Q8ezd0 leptospira
Q8yan8 listeria mo
Q9wbt0 human immun
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<b>.</b> 4 5	44	43	42	41	40	39	38	37	36	<b>3</b> 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
36	36	36	36		36	36	36	36	36.5	37	37	37	37	37	37	37	37	37	37	37	37	ა 8	38	38	38	38	38	39
49.3	49.3				49.3	•		49.3	50.0	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	52.1	52.1	52.1	52.1	52.1	52.1	53.4
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Q9A0P6	Q97WK1	Q8KZ35	QBISSB	Q92JI8	Q8Z491	Q966I8	Q97KU4	Q8MK94	076506	Q9BIX3	Q18901	Q8IB98	Q8DT19	Q9T1E3	Q9M6E6	030857	Q8KJ83	Q973X9	037154	Q9Q3U7	010689	Q8IKQ8	Q8BSJ2	Q9B8G9	Q8CXK7	Q9TSN4	Q20029	Q12180
Q9a0p6 streptococc	Q97wk1 sulfolobus	Q8kz35 uncultured	Q8iss8 leishmania	Q92ji8 rickettsia	Q8z491 salmonella	Q966i8 caenorhabdi	Q97ku4 clostridium					ю.		Q9tle3 lactobacill		O30857 vibrio chol.	Q8kj83 rhizobium l	w	O37154 cymbidium m		Ol0689 cymbidium m		N	Q9b8g9 heterodoxus	7	Q9tsn4 macaca fasc	Q20029 caenorhabdi	Q12180 saccharomyc

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B. 8	Quer Best Matcl	SQ K R	RA DR	R R RN	R R R R	8 R S S	000025		RESULT O14042 ID O
1 DSEMYNFRSQLAS  :      :    176 DTEMSNFRTQLAS	Query Match Best Local Similarity 76. Matches 10; Conservative	GeneDB_Spombe; SPAC2C4.09; Hypothetical protein. SEQUENCE 216 AA; 25318 P	'n	[2] SEQUENCE FROM N.A. STRAIN=972h-	STRAIN-972h; STRAIN-972h; Oliver K., Harris D.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases	Schizosaccharomyces. NCBI_TaxID=4896; [1]	SPACZC4.09. SPACZC4.09. Schizosaccharomyces pombe (Fission yeast). Schizosaccharomyces pombe (Fission yeast). Schizosaccharomycetes Schizosaccharomycetales; Schizosaccharomycetaceae;		LT 1 42 014042 PRELIMINARY;
)LAS 13   }    AS 188	5%; Scc 9%; Pre 2;	5318 MW;	Rajandream M.A., Wood V.; -1997) to the EMBL/GenBar CAB16369.1;		).; // to the EMBL/Ge	, w	compces pombe (Fission yeast) ngi; Ascomycota; Schizosacch comycetales; Schizosaccharomy	08, Crea 08, Last 23, Last	INARY; PRT;
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MEDLINE=22404279; PubMed=12516573;

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MEDILINE=22404279; PubMed=12516573;

Kurth J., Pernick A., Schmitz R., Iking-Konert C., C.

Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;

"Lack of deleterious somatic mutations in the CD95 g
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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EMBL; AJ509181; CAD48931.1; -.
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RESULT 5
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Best Local S
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Q9BYF1;
01-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                      InterFro; IPR001548; Peptidase M2.
InterFro; IPR006025; Zn_MTpeptdse.
Pfam; PF01401; Peptidase M2; 1.
PRINTS; PR00791; PEPDIPTĀSEA.
PRODOM; PD004184; Peptidase M2; 1.
PROSTTE; PS00142; ZINC_PROTEASE; 1.
SEQUENCE 805 AA; 92491 MW; D2AAB4C27088EB72
                                                                                                                                                                                                                                      MEROPS; M02.006; -. Genew; HGNC:13557; ACE2.
                                                                                                                                                                                                                                                                                                     Submitted (APR-2001) to the
                                                                                                                                                                                                                                                                                                                        "Cloning, expression 
ACE like enzyme.";
                                                                                                                                                                                                                                                                                                                                                           Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
NON TER 1
SEQUENCE 804 AA; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00791; PEPDIPTASEA.
PRODOM; PD004184; Peptidase M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wambutt R., Heubner D., Mew Submitted (AUG-1999) to the EMBL; AL110224; CAB53682.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein DKFZP434A014.
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                                                                                                                                                                                                                                                                                  EMBL; AB046569; BAB40370.1;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               Komatsu T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006025; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [nterPro; IPR001548; Peptidase_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; M02.006; -.
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Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                    Watanabe M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 17, (TrEMBLrel. 17, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM N.A.
Suzuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
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Primates;
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66.7%;
                                                                                                                                                                                                                                                                                                                                            M., Sugano S.;
analysis and
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                              56.2%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sugano S.;
o the EMBL/GenBank/DDBJ
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                              Score 41;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91FF391074CB5DA9 CRC64;
            Mismatches
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nBank/DDBJ databases.
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          2;
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                                                 Length 805;
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RESULT 7
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Best Local S
Matches 8
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Q9W5S5;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, I
01-MAY-2000 (TrEMBLrel. 13, I
CG17506 protein.
STRAIN-BERKELEY;
MEDLINE-20196006;
                                                                                                                              Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carboxypeptidase.
SEQUENCE 805 AA
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InterPro; IPR006025; Zn MTpeptdse.
Pfam; PF01401; Peptidase M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
ProDom; PD004184; Peptidase M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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EMBL; AF291820; AAF99721.1;
MEROPS; MO2.006;
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Circ. Res. 0:0-0(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stagliano N., D
Breitbart R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tipnis S.R., Hooper N.M., Hyde R.J., Christie G., Turner A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiotensin converting enzyme-like carboxypeptidase ACE2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9NRA7;
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                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M., Hsieh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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   PubMed=10731132;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92462 MW;
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Last sequence update)
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me-like protein (ACE-related
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Pred. No. 53;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Jeyaseelan R.
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RA Ballew R.M., Baros P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu S., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodeon K., Doup E.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodeon K., Doup F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Meshrefi A.,
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Meshrefi A.,
RA Merkulov G., Milehon K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Ralezzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,
RA Ralezzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,
RA Ralezzolo M., Siden K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Siden K.A., Nixon K., Supski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Moodege T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Moodege T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhang G., Zhao Q., Zheng L.,
RA Milliams S.M., Moodege T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Kalus S., Mandra S., Randra S., Jan W., Smith H.O.,
RA Milliams S.M., Moodege T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
RA Mandra S.M., Mo
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01-OCT-2001
                   SEQUENCE FROM N.A.

STRAINATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Alla Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtip De Moors A., Erause G., Fletcher C., Gordon P.M.K., Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina
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                                                                                                                                                                                                                  Archaea; Crenarchaeota; Sulfolobus.
                                                                                                                                                                                                                                                         Sulfolobus
                                                                                                                                                                                                                                                                             Hypothetical SS01545.
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Pred. No.
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Theriault C., Tolstrup N.,
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Best Local
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Best Local (
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                                                                 Ol-Mar-2003 (TrEMBLrel. 23, Labrand Martin M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       022397;
01-JAN-1998
01-JAN-1998
01-MAR-2003
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"The complete genome of the crenarchaeon Sulfolobus solfataricus Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

EMBL; AE006769; AAK41763.1; -.
InterPro; IPR004309; DUF238.
Pfam; PF03075; DUF238; 1.

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete proteome.
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"A new family of K+ transporters across phyla.";
FEBS Lett. 415:206-211(1997).
[1] T
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                    050043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     050043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003855; K+_transporter.
Pfam; PF02705; K trans; 1.
TIGREAMS; TIGR00794; kup; 1.
SEQUENCE 712 AA; 79032 MW; BF766
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EMBL; AF012656; AAC49844.1; -.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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nsporter (High affinity
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RESULT 11
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Town C.D., Kaul S.;
Submitted (FBE-2002) to the EMBI
EMBL; AF029876; AAB88901.1; -.
EMBL; AF033118; AAB87687.1; -.
EMBL; AC004165; AAC16965.1; -.
EMBL; AC004680; AAM14984.1; -.
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Q92JC5;
01-DEC-2001
01-DEC-2001
01-MAR-2003
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SEQUENCE
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Submitted
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                        EMBL; AB008581; AAL02680.1; -.
InterPro; ITR001092; HLH basic.
PROSITE; PS00038; HLH 1; 1.
Hypothetical protein; Complete
SEQUENCE 993 AA; 108744 MW;
                                                                                                                  MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P.,
Samson D., Roux V., Cossart P., Weissenbac
Raoult D.;
                                                                                              "Mechanisms of evolution in Rickettsia Science 293:2093-2098(2001).
                                                                                                                                                               STRAIN=Malish
                                                                                                                                                                                                       Rickettsiaceae;
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Pfam; PF02705; K trans; 1.
TIGREAMs; TIGR00794; kup; 1.
SEQUENCE 712 AA; 79126 MW; 0FE32
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Last annotation update)
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Pred. No.
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Q9ZE44
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                                      Nat. E
EMBL;
                                                                                                    Heidelberg J.F., Paulsen I.T., Neison K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Desby R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Wanathevan J., Waidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.K., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shewanella oneidensis
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01-MAR-2003
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EMBL; AJ235270; CAA14573.1; -.

InterPro; IPRO01092; HLH basic.

PROSITE; P800038; HLH 1; 1.
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Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia prowazekii.
Bacteria; Proteobacteria; Alph
Rickettsiaceae; Rickettsieae;
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1124 AA; 124974 MW; EAC1E61564734EEB CRC64;
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Q8EZDO;
01-MAR-2003
                                                      Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perca-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE011548; AAN51122.1; -.
Oxidoreductase; Complete proteome
SEQUENCE 321 AA; 35515 MW; OB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes.
Bacteria; Firmicutes; E
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STRAIN=56601 / 8
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NCBI_TaxI
                  Science 294:849-852(2001).
EMBL; AL591973; CAC98294.1;
                                                                                                                                                                                                                                                                                                                                    MEDLINE=21537279;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1639;
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Bacteria; Spirochaetes;
NCBI_TaxID=173;
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